GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3229.12 Seconds
                                              (without alignments)
                                              10265.033 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc..........ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                  1:   em_estba:*
                  2:   em_esthum:*
                  3:   em_estin:*
                  4:   em_estmu:*
                  5:   em_estov:*
                  6:   em_estpl:*
                  7:   em_estro:*
                  8:   em_htc:*
                  9:   gb_est1:*
                  10: gb_est2:*
                  11: gb_htc:*
                  12: gb_est3:*
                  13: gb_est4:*
                  14: gb_est5:*
                  15: em_estfun:*
                  16: em_estom:*
                  17: em_gss_hum:*
                  18: em_gss_inv:*
                  19: em_gss_pln:*
                  20: em_gss_vrt:*
                  21: em_gss_fun:*
                  22: em_gss_mam:*
                  23: em_gss_mus:*
                  24: em_gss_pro:*
                  25: em_gss_rod:*
                  26: em_gss_phg:*
                  27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729.2	65.7	1740	11	BC035686	BC035686 Homo sapi
c 2	696	62.7	886	13	BX433093	BX433093 BX433093
c 3	650.4	58.6	899	13	BX433092	BX433092 BX433092
4	554.4	49.9	753	29	AY420885	AY420885 Homo sapi
5	521.4	47.0	3470	11	AK048781	AK048781 Mus muscu
6	521.4	47.0	3729	11	AK038551	AK038551 Mus muscu
7	511.8	46.1	1790	11	BC035858	BC035858 Homo sapi
8	510.4	46.0	3153	11	AK079572	AK079572 Mus muscu
c 9	500.6	45.1	790	14	CF147830	CF147830 AGENCOURT
10	467.2	42.1	750	29	AY420886	AY420886 Pan trogl
11	462.4	41.7	726	29	AY420887	AY420887 Mus muscu
12	462.4	41.7	1001	9	AL535838	AL535838 AL535838
13	385.2	34.7	993	12	BM926746	BM926746 AGENCOURT
14	376.2	33.9	543	13	BX119589	BX119589 BX119589
15	359	32.3	788	14	CF147829	CF147829 AGENCOURT
16	322.8	29.1	382	12	BQ042116	BQ042116 sheep1 Sh
c 17	288	25.9	525	12	BI133700	BI133700 UI-M-BH3-
18	280.6	25.3	635	12	BM939496	BM939496 UI-M-BH3-
19	277.8	25.0	520	13	BQ269289	BQ269289 ik23f12.y
20	264.2	23.8	627	10	BB632359	BB632359 BB632359
21	263.8	23.8	599	12	BM933820	BM933820 UI-M-BH3-
22	261.6	23.6	611	13	BY723922	BY723922 BY723922
23	248.4	22.4	892	13	BX409735	BX409735 BX409735
24	208.8	18.8	477	12	BM087401	BM087401 500158 MA
25	200.8	18.1	662	10	BB632883	BB632883 BB632883
26	199.8	18.0	1073	12	BM920548	BM920548 AGENCOURT
c 27	197.8	17.8	625	13	BQ285933	BQ285933 ik23f12.x
28	197.6	17.8	505	10	BB651179	BB651179 BB651179
29	195.2	17.6	245	12	BI976482	BI976482 485407 MA
30	186.2	16.8	464	13	BY239887	BY239887 BY239887
31	177	15.9	444	14	R55704	R55704 yg88h10.r1
c 32	164.2	14.8	703	29	CE375359	CE375359 tigr-gss-
33	162	14.6	721	29	CE235359	CE235359 tigr-gss-
34	161.6	14.6	1290	29	AY411591	AY411591 Homo sapi
35	156.2	14.1	1296	29	AY411593	AY411593 Mus muscu
c 36	155.6	14.0	1013	9	AL535837	AL535837 AL535837
37	146.2	13.2	768	13	BX109847	BX109847 BX109847
38	133	12.0	257	10	AW427900	AW427900 64510 MAR
39	120.2	10.8	526	29	CG978334	CG978334 CH240_169
c 40	119.2	10.7	1005	28	CC212654	CC212654 CH261-75F
c 41	119.2	10.7	1058	28	CC297061	CC297061 CH261-177
42	117.4	10.6	1113	29	AY420480	AY420480 Homo sapi
43	115.4	10.4	1100	29	AY420481	AY420481 Pan trogl
c 44	114.4	10.3	1194	28	CC279941	CC279941 CH261-24C
45	108.8	9.8	1113	29	AY420482	AY420482 Mus muscu

RESULT 1
BC035686

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LOCUS       BC035686                1740 bp    mRNA    linear   HTC 20-SEP-2002
DEFINITION  Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone
            IMAGE:5750551, mRNA.
ACCESSION   BC035686
VERSION     BC035686.1  GI:23242909
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1740)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: m Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4557636
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .1740
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5750551"
                     /tissue_type="Lung, Spleen, fetal, pooled"
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ORIGIN

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Query Match            65.7%;  Score 729.2;  DB 11;  Length 1740;
Best Local Similarity  83.2%;  Pred. No. 4e-138;
Matches  923; Conservative   0;  Mismatches   8;  Indels 179;  Gaps   1;
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Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     506 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 565

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db     626 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 685

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           ||||||||||||||||||
Db     686 CTGGTGGGCAACACGCTG------------------------------------------ 703

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Db     704 --------------------------------------------------------- 703

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Db     704 --------------------------------------------------------- 703

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                           ||||||||||||||||||||||||||||||||||||||||||||
Db     704 -----------------GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     747 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 806

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     807 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 866

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           ||||||||| |||  |||||||||||||||||||||||||||||||||||||||||||||
Db     867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     927 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 986

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     987 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 1046
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Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db      1047 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 1106

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      1107 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 1166

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1226

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db      1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db      1287 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1406

Qy      1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
             ||||||||||||||||||||||||||||||
Db      1407 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1436
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RESULT 2
BX433093/c

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LOCUS       BX433093                886 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433093
VERSION     BX433093.1  GI:30779168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
  COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_2.
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FEATURES                 Location/Qualifiers
     source              1. .886
                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="CS0DF013YE04"
                         /tissue_type="FETAL BRAIN"
                         /dev_stage="fetal"
                         /clone_lib="Homo sapiens FETAL BRAIN"
                         /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                         was primed with a NotI-oligo(dT) primer. Five prime end
                         enriched, double-strand cDNA was digested with Not I and
                         cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                         vector. Library was not normalized."
ORIGIN

   Query Match            62.7%;   Score 696;   DB 13;   Length 886;
   Best Local Similarity  98.5%;   Pred. No. 1.7e-131;
   Matches  702;  Conservative   0;  Mismatches  11;  Indels  0;  Gaps  0;


Qy       377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGT 436
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Db       745 AGGCTGTGTCCGTGTCAGTGACAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 686

Qy       437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATNC 626

Qy       497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCA 556
             |||||||||| |||||||||||||||||||||||||   |||||||||||||||||| ||
Db       625 TGGGCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCAGGGCTGCAGTCATGCAATGCA 566

Qy       557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCT 616
             |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db       565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 506

Qy       617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
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Qy       677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
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Db       445 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 386

Qy       737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 796
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Db       385 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 326

Qy       797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTG 856
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTG 266

Qy       857 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       265 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 206

Qy       917 TCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA 976
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              | | | | | | | | | | | | | | | | | | | | | | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      205   TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA 146

Qy      977   TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 1036
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Db      145   TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 86

Qy     1037   TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGC 1089
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       85   TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGC 33
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RESULT 3
BX433092/c
LOCUS   BX433092   899 bp   mRNA   linear   EST 15-MAY-2003
DEFINITION   BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
              CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433092
VERSION   BX433092.1 GI:30779167
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 899)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 151.r For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
              Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.
FEATURES   Location/Qualifiers
     source   1. .899
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                       /db_xref="taxon:9606"
                       /clone="CS0DF013YE04"
                       /tissue_type="FETAL BRAIN"
                       /dev_stage="fetal"
                       /clone_lib="Homo sapiens FETAL BRAIN"
                       /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                       was primed with a NotI-oligo(dT) primer. Five prime end
                       enriched, double-strand cDNA was digested with Not I and
                       cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                       vector. Library was not normalized."
ORIGIN

   Query Match   58.6%; Score 650.4; DB 13; Length 899;
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Best Local Similarity  94.0%;  Pred. No. 3.5e-122;
Matches  686;  Conservative  0;  Mismatches  43;  Indels  1;  Gaps  1;

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Qy      372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCG 431
            | ||    |||||||   |||||||||||||||| |||||||||||| ||  |   |||
Db      738 TGTAAGNNCTGTGTCGTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy      432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCT 490
            ||||||||||||| | |||||||||||||||| |||||||||||||||||||||||||||
Db      678 CTGGTATGCCATCATCCCACCCACTATTGTCAAAGAGCACAGCCCGGCGGGCCCGTGCTC 619

Qy      491 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGC 550
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      618 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 559

Qy      551 AATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATG 610
            |||  ||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db      558 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 499

Qy      611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 670
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 439

Qy      671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 730
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 379

Qy      731 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 790
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      378 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 319

Qy      791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 850
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      318 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCC 259

Qy      851 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      258 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199

Qy      911 TGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db      198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139

Qy      971 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      138 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79

Qy     1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCC 1090
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Db       78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTCAACTTCCTCAGGTGCAA 19

Qy     1091 TTCCCTGGAG 1100
            | || ||||
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RESULT 4

AY420885

LOCUS   AY420885   753 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY420885
VERSION   AY420885.1 GI:39776842
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence as made by sequencing genomic exons and ordering them
             based on alignment.
FEATURES   Location/Qualifiers
     source   1. .753
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1. .>753
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

     Query Match   49.9%; Score 554.4; DB 29; Length 753;
     Best Local Similarity   98.9%; Pred. No. 1.2e-102;
     Matches 558; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
            ||||||||||| ||||||||||||||| ||| ||||||||||||||||||||||||||||
Db   1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy   586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
            ||||||||||||||| |||||| |||||||||||||||||||||||||||||||||||||
Db   61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy   646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy   706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765

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Db       181    TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy       766    CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
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Qy       826    CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Qy       886    ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
                ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
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Qy       946    GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
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Qy       1006   GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
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Qy       1066   ATCATCTACAACTTCCTCAGTGGC 1089
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Db       541    ATCATCTACAACTTCCTCAGTGGC 564
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RESULT 5
AK048781
LOCUS       AK048781                3470 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK048781
VERSION     AK048781.1  GI:26339571
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
```

                    Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
                    Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
                    Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
                    Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
                    Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
                    Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
                    sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
                    FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
                    Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
                    of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3470)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                    Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
                    Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
                    Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
                    Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
                    Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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                    Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                    Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
                    Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                    Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                    Physical and Chemical Research (RIKEN), Laboratory for Genome
                    Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                    RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                    Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                    URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                    Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
                    Encyclopedia Project of Genome Exploration Research Group in Riken
                    Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                    Division of Experimental Animal Research in Riken contributed to
                    prepare mouse tissues.
                    Please visit our web site for further details.
                    URL:http://genome.gsc.riken.go.jp/
                    URL:http://fantom.gsc.riken.go.jp/.
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    Qy          80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
                    I II II II II II II II IIIIII I II II II  IIII III I IIIIIII
    Db         178 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 237

    Qy         140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
                    IIIIIII IIIIIII  III I      IIIIIIIII IIIII II  I II III   IIII
    Db         238 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 297

    Qy         200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
                    IIII  IIII IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII IIII
    Db         298 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 357

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                    IIII IIIII II II II II IIIII    I IIIIII II II I III I II I
    Db         358 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 417

    Qy         320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Qy    440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Qy    680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Qy    800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Qy    860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Qy    980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
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Qy   1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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Db   1132 TATATGCCAACAGTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG 1180
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RESULT 6
AK038551

            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
    TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
    TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
    TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
    TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
    TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3729)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
    TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

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COMMENT         cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues.
                Please visit our web site for further details.
                URL:http://genome.gsc.riken.go.jp/
                URL:http://fantom.gsc.riken.go.jp/.
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     Matches   712;  Conservative    0;  Mismatches  291;  Indels    6;  Gaps    1;


Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db        179 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 238


Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db    239 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 298

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Qy    260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db    359 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 418

Qy    320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Qy    380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
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Qy    440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db    539 CCATTTGTCACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 598

Qy    500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
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Db    599 TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA 658

Qy    560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
           |    |||| ||||   ||||||||       ||    |||||| || | ||| ||||| | |||||
Db    659 GCATGCTCCCTGGCCTAGCCAATAAGACCACCCTCTTTACAGTATGTGATGAACACTGGG 718

Qy    620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
           |  |||  | || || |||||  |||||     |||||||||| | || || |||  |||| |
Db    719 GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC 778

Qy    680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
           |  ||| | || |||      |||| |||| |||| |||||||| || ||||||| |||| ||||
Db    779 CTCTGTGTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA 838

Qy    740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
            | ||||| ||  | || |     |  | | || |||||||| |     | ||||| ||
Db    839 TTCCCGGAACTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC------AGCAGCCGGTTT 892

Qy    800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
           | |   | ||| |     |  | || | || |||  ||| | | | |||| |    ||||
Db    893 CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGATTAGCGCTGTTGCTGCTGAGA 952

Qy    860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
           | ||||||||| || |||||| |||||| ||||||||||| |||||| ||| || |||||||
Db    953 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1012

Qy    920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
            | ||   | ||||| || || |||||||||||||||| || || || || || |||||||
Db   1013 TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1072

Qy    980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCCTTCACCTTCTCCCACTGGCTGG 1039
           ||   || |    ||| | || |||||||||| || || ||||| || || || |||||| |
Db   1073 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTTTCTCATTGGCTTG 1132
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Qy    1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
           |  ||  ||||||||  |||||  |||||  ||  ||  ||  ||  ||  ||  |||||
Db    1133 TATATGCCAACAGTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG 1181
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RESULT 7
BC035858
LOCUS   BC035858   1790 bp   mRNA   linear   HTC 04-MAR-2003
DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone
            IMAGE:5767576, mRNA.
ACCESSION   BC035858
VERSION   BC035858.1 GI:23959160
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1790)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: p Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006037
            This clone has the following problem: retained intron.
FEATURES   Location/Qualifiers
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       Qy       80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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       Db      206 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 265

       Qy      200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
                     | ||  |||| |||||| |||||||||||||||||||||| || |||||||||||| ||||
       Db      266 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 325

       Qy      260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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       Db      326 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 385

       Qy      320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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       Db      386 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 445

       Qy      380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
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       Qy      440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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       Db      506 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 565

       Qy      500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
                     ||||||| ||| ||   || ||| | || |||||   |||||| | | |||||
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       Qy      560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
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RESULT 8
AK079572
LOCUS       AK079572                3153 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK079572
VERSION     AK079572.1  GI:26348079
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
 PUBMED     11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3153)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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     Best Local Similarity   70.5%;   Pred. No. 2.2e-93;
     Matches 712; Conservative   0; Mismatches 291; Indels   7; Gaps   2;

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             I II II II II II II II IIIIII I II·II II IIII III I IIIIIII
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Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Qy   200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Db   331 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 390

Qy   260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Qy   380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
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Qy   440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db      751  GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC  810

Qy      680  CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA  739
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Qy      860  TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT  919
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Qy      920  TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT  979
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Db     1045  TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT  1104

Qy      980  TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG  1039
             ||   || |   ||| | ||  ||||||| || || ||||| || | || ||||| |
Db     1105  TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTCCTCATTGGCTTG  1164

Qy     1040  TGTACGCCAACAGC-GCTGCCAACCCCATCATCTACAACTTCCTCAGTGG  1088
             | || |||||||| ||||| ||||| || || || || || || |||||
Db     1165  TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG  1214
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RESULT 9
CF147830/c
LOCUS   CF147830   790 bp   mRNA   linear   EST 25-JUL-2003
DEFINITION   AGENCOURT_14740202 NIH_MGC_145 Homo sapiens cDNA clone
              IMAGE:6971889 5', mRNA sequence.
ACCESSION   CF147830
VERSION   CF147830.1 GI:33244098
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 790)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: GPCR Consortium
              cDNA Library Preparation: GPCR Consortium

FEATURES   Location/Qualifiers
     source   1. .790
                          /organism="Homo sapiens"
                          /mol_type="mRNA"
                          /db_xref="taxon:9606"
                          /clone="IMAGE:6971889"
                          /tissue_type="mixed"
                          /lab_host="DH10B"
                          /clone_lib="NIH_MGC_145"
                          /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                          varies by clone; ORFs were PCR-amplified and cloned into
                          pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                          clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                          5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                          For information about which gene each clones represents,
                          please visit our anonymous ftp site at
                          ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                          a Note: this is a NIH_MGC Library."
     ORIGIN

  Query Match   45.1%; Score 500.6; DB 14; Length 790;
  Best Local Similarity   99.2%; Pred. No. 1.2e-91;
  Matches 503; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   583 CGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 642
              ·||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db   790 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 731

Qy   643 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   730 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671

Qy   703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611

Qy   763 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   610 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551

Qy   823 GAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 882
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   550 GAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 491

Qy   883 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATC 942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   490 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 431

Qy   943 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 1002

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                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371


Qy       1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311


Qy       1063 CCCATCATCTACAACTTCCTCAGTGGC 1089
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Db        310 CCCATCATCTACAACTTCCTCAGTGGC 284
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RESULT 10
AY420886
LOCUS   AY420886   750 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Pan troglodytes HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420886
VERSION   AY420886.1 GI:39776843
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES   Location/Qualifiers
     source   1. .750
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1. .>750
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

  Query Match   42.1%;   Score 467.2; DB 29; Length 750;
  Best Local Similarity 83.7%;   Pred. No. 7.6e-85;
  Matches 472; Conservative   0; Mismatches 92; Indels   0; Gaps   0;
```

```
Qy    526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
          ||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||
Db      1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy    586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
          |||||||||||||| ||||| |||||||||||||||||||||||||||||||||||||||
Db     61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy    646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy    706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy    766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy    826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
          ||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||
Db    301 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCGCGGAGGAAG 360

Qy    886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGT 420

Qy    946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
          |||||||||||||||||||||
Db    421 GTCCTCAATGTCCTTAAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Qy   1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
                                                   |||||||||      |||||||||
Db    481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACGCCAACAGNNNGCCAACCCC 540

Qy   1066 ATCATCTACAACTTCCTCAGTGGC 1089
          ||||     ||||||||||||||||
Db    541 ATCANNNACAACTTCCTCAGTGGC 564
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RESULT 11
AY420887

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LOCUS       AY420887                726 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420887
VERSION     AY420887.1  GI:39776844
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
```

                        Adams,M.D. and Cargill,M.
        TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
                    gene trios
        JOURNAL   Science 302 (5652), 1960-1963 (2003)
        PUBMED   14671302
    REFERENCE   2   (bases 1 to 726)
        AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                    Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                    Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                    Adams,M.D. and Cargill,M.
        TITLE   Direct Submission
        JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                    Rockville, MD 20850, USA
    COMMENT   This sequence as made by sequencing genomic exons and ordering them
                    based on alignment.
    FEATURES   Location/Qualifiers
        source   1. .726
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10090"
        gene   <1. .>726
                    /gene="HCRTR1"
                    /locus_tag="HCM7373"
    ORIGIN

      Query Match   41.7%;   Score 462.4; DB 29; Length 726;
      Best Local Similarity   87.0%;   Pred. No. 7.2e-84;
      Matches 508; Conservative   0; Mismatches   76; Indels   0; Gaps   0;

Qy   526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
             ||||||||||||||||| ||||||| | | ||||||| ||||||||||||||||||| |||
Db   1 ATGGTGCCCCAGGCTGCTGTCATGGAGTGCAGCAGCGTGCTGCCTGAGCTAGCCAATCGC 60

Qy   586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
             || |||||||||||| ||||| ||||| | |||||||||||| ||||| |||||||||||
Db   61 ACCCGGCTCTTCTCTGTCTGTGATGAGCACTGGGCAGATGAACTCTACCCCAAGATCTAT 120

Qy   646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
             ||||| |||||| || |||||||||||||||||||||||||||||||||| |||||||||
Db   121 CACAGCTGCTTTTTCATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCTATGGCCTAT 180

Qy   706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
             |||||||| |||||||||||||||||||||||||||||||| || ||||| ||||| |||||
Db   181 TTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGTACCACATCAGCCTTGGTG 240

Qy   766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
             ||||||||||| || ||||| || || |||| || | | | ||||||| || ||||
Db   241 CGGAACTGGAAACGGCCCTCGGAACAACTGGAGGCTCAGCACCAGGGCCTCTGTACAGAG 300

Qy   826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
             ||||||||||||| ||| ||||||||||||||| ||||||||||||| || |||||||||
Db   301 CCCCAGCCCCGGGCCCGAGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG 360

Qy   886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
             || || |||||||||||||| || |||||||| || || ||||| || || |||||||||
Db   361 ACGGCTAAGATGCTGATGGTAGTCCTGCTGGTTTTTGCACTCTGTTATCTGCCCATCAGT 420

```
Qy    946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
          |||||||||||||||||||||| |+|||||||||||||||+|||||||| ||||| |||||
Db    421 GTCCTCAATGTCCTTAAGAGAGTGTTCGGGATGTTCCGCCAAGCCAGCGACCGGGAAGCC 480

Qy   1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
          |||||||||||||||||||||||||||||||||| ||||||||||||| || |||||||||
Db    481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTAGTGTACGCCAACAGTGCCGCCAACCCT 540

Qy   1066 ATCATCTACAACTTCCTCAGTGGCCTTCCCTGGAGTCTGCTCTA 1109
          ||||||||||||||||||||||||||      | ||   | ||| |
Db    541 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTCAA 584
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RESULT 12
AL535838

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LOCUS       AL535838                1001 bp    mRNA    linear    EST 12-MAY-2003
DEFINITION  AL535838 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 5-PRIME, mRNA sequence.
ACCESSION   AL535838
VERSION     AL535838.2  GI:30542758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12799331.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.
FEATURES             Location/Qualifiers
     source          1. .1001
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF013YE04"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
```

```
Query Match              41.7%;  Score 462.4;  DB 9;  Length 1001;
Best Local Similarity    91.0%;  Pred. No. 8.3e-84;
Matches  538;  Conservative  13;  Mismatches  31;  Indels  9;  Gaps  6;

Qy    377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGT 436
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Db    415 AGGCTGTGTCCGTGTCANTGGCAGTGCTAACTCTMANCTTCATCGCMCTGGACCGCTGGT 474

Qy    437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
          ||||:||||||:|||||||||||||||||||||:||||||||||||||||||||||||||
Db    475 ATGCHATCTGCYACCCACTATTGTTCAAGARCACAGCCCGGCGGGCCCGTGGCTCCATCC 534

Qy    497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCA 556
          |  | ||||||||| | |||||||||||||||||||||||||||||||||||| ||| ||
Db    535 TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 594

Qy    557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCT 616
          |||||||||||||| ||||| |||||||||||||||||||||||| ||||| ||||||||
Db    595 GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 654

Qy    617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 714

Qy    677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 774

Qy    737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCT-G 795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    775 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 834

Qy    796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCT 855
          |||||||||||||||||||||||||||||||||||    ||| |||||||||||||||||
Db    835 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCC--AGCCCCGGGCCGCGCCTTCCTGGCT 892

Qy    856 GAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTG 915
          |||||||   : |   |   ||  |:|||||:|:|||||||||||||||||||:|||||||
Db    893 GAAGTGA---RCAGATGSTGCAGGCAGVAGACASCSAAGATGCTGATGGTGGBGCTGCTG 949

Qy    916 GTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGG 966
          :||||||| |||||||||:| ||||||||:|| |||||||||| | ||||||
Db    950 STCTTCG-CCTCTGCTACST-GCCATCAGSGT-CTCAATGTCTTAAAGAGG 997
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RESULT 13
BM926746

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LOCUS       BM926746              993 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6681991 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767576
            5', mRNA sequence.
ACCESSION   BM926746
VERSION     BM926746.1  GI:19377125
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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```
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 993);
  AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
    TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL       Unpublished (1999)
  COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Life Technologies, Inc.
                 cDNA Library Preparation: Life Technologies, Inc.
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Agencourt Bioscience Corporation
                 Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM12826  row: a  column: 17
                High quality sequence stop: 684.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5767576"
                      /lab_host="DH10B"
                      /clone_lib="NIH_MGC_121"
                      /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                      fetal brains, female age 20 weeks, female age 24 weeks,
                      and male age 26 weeks.  Library is oligo-dT primed and
                      directionally cloned (EcoRV site is destroyed  upon
                      cloning).  Average insert size 1.7 kb, insert size range
                      0.7-3.5 kb.  Library is normalized and enriched for
                      full-length clones and  was constructed by C. Gruber
                      (Invitrogen).  Research Genetics  tracking code 017. Note:
                      this is a NIH_MGC Library."
ORIGIN

     Query Match          34.7%;  Score 385.2;  DB 12;  Length 993;
     Best Local Similarity 71.4%;  Pred. No. 4.6e-68;
     Matches  507;  Conservative   0;  Mismatches  203;  Indels   0;  Gaps   0;

Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || | |||||| | || || ||| |||| ||| | |||||||
Db       145 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 204

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| |||||| | || | |||||i|||||||| || | || |||    ||||
Db       205 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 264

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||   |||| |||||| |||||||||||||||||| || |||||||||||||| ||||
Db       265 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 324

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || ||||||||| || || ||||| | |||||| || |||| ||| | ||||
Db       325 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 384

Qy      .320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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           |  |||||||||| |||||| | || || ||  |||| ||||| || || || |||||||||||
Db    385  ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA  444

Qy    380  CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG  439
           | |||||| |||||| ||| | | || || || || |||| ||| || |||| || |||||||
Db    445  CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG  504

Qy    440  CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG  499
           | |||||| |||||| | |||| ||||||||||| ||||||||||| | ||| |
Db    505  CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA  564

Qy    500  GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA  559
           ||||||| ||| || || || ||| | || ||||| |||||| | | |||||
Db    565  TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA  624

Qy    560  GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG  619
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Db    625  CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG  684

Qy    620  CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC  679
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Db    685  GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC  744

Qy    680  CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA  739
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Db    745  CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA  804

Qy    740  TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGAC  789
           |||| || || | || | | | | |||| ||||| ||| || |
Db    805  TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAAGCCCCTGGAGCC  854
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RESULT 14
BX119589

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LOCUS        BX119589               543 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION   BX119589 Soares infant brain 1NIB Homo sapiens cDNA clone
             IMAGp998P20171 ; IMAGE:40608, mRNA sequence.
ACCESSION    BX119589
VERSION      BX119589.1  GI:28289997
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 543)
  AUTHORS    Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
             Radelof,U., Schneider,D. and Korn,B.
  TITLE      Human UnigeneSet - RZPD3
  JOURNAL    Unpublished (2003)
COMMENT      Contact: Ina Rolfs
             RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
             RZPD; IMAGp998P20171.
             RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
             Human UnigeneSet - RZPD3 (RZPDLIB No.972)
             http://www.rzpd.de/CloneCards/cgi-
             bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
```

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FEATURES              Location/Qualifiers
     source           1. .543
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGp998P20171 ; IMAGE:40608"
                      /sex="female"
                      /dev_stage="73 days post natal"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares infant brain 1NIB"
                      /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                      I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                      I - oligo(dT) primer [5'
                      AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTTT 3'];
                      double-stranded cDNA was ligated to Hind III adaptors
                      (Pharmacia), digested with Not I and directionally cloned
                      into the Not I and Hind III sites of the Lafmid BA vector.
                      Library went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
     ORIGIN
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   Query Match            33.9%;  Score 376.2;  DB 13;  Length 543;
   Best Local Similarity  99.0%;  Pred. No. 2.4e-66;
     Matches  378;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      158 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 217

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      218 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 277

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      278 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 337

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      338 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 397

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      398 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 457

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      458 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGNAAG 517
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Qy      361  GTCATCCCCTATCTACAGGCTG 382
             |||||||||||·|||||||| | |
Db      518  GTCATCCCCTATCTACAGACAG 539
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RESULT 15
CF147829
LOCUS   CF147829   788 bp   mRNA   linear   EST 25-JUL-2003
DEFINITION   AGENCOURT_14740210 NIH_MGC_145 Homo sapiens cDNA clone
              IMAGE:6971890 5', mRNA sequence.
ACCESSION   CF147829
VERSION   CF147829.1 GI:33244097
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: GPCR Consortium
               cDNA Library Preparation: GPCR Consortium
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: IRBI02 row: a column: 09
              High quality sequence start: 9
              High quality sequence stop: 772.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971890"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_145"
                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

     Query Match   32.3%; Score 359; DB 14; Length 788;
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Best Local Similarity   72.0%;   Pred. No. 9.2e-63;
Matches  467;  Conservative     0;  Mismatches  182;  Indels    0;  Gaps    0;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || || |||||| | || || ||| |||| ||| | ||||||||
Db       140 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 199

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| |||||| | || |     ||||||||||||||| || | || ||||    ||||
Db       200 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 259

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              | ||    |||| |||||||     |||||||||||||||||| || |||||||||||||| ||||
Db       260 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 319

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              | || || |||||||| || || |||||       | |||||| || |||| ||| | ||||
Db       320 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 379

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              | |||||| ||| |||||| | || || || |||| ||||| || || || |||||||||
Db       380 ATATCACCGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 439

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              | ||||| ||||| ||| | | || || || || |||| ||| || |||| || |||||||
Db       440 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 499

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              | |||||| |||||     |||| |||||||||||||||| ||||||||||| | ||| |
Db       500 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 559

Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
               ||||||| ||| || || || ||| | || |||||     |||||| | | ||||||
Db       560 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 619

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
              |||| | || |   ||||||| || ||||| | | ||| |||| |||||||
Db       620 CTGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 679

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  | |||||||||||||| ||||||| || |||||| | || || ||| |||| |
Db       680 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 739

Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTG 728
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Db       740 CACTGTGTCTCATGGTGTTGGCTTATCTGNCAATATTTCGCANACTCTG 788
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Search completed: October 15, 2004, 22:50:30
Job time : 3232.12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 4497.38 Seconds
                                             (without alignments)
                                             10697.520 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc..........ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
           1:    gb_ba:*
           2:    gb_htg:*
           3:    gb_in:*
           4:    gb_om:*
           5:    gb_ov:*
           6:    gb_pat:*
           7:    gb_ph:*
           8:    gb_pl:*
           9:    gb_pr:*
          10:    gb_ro:*
          11:    gb_sts:*
          12:    gb_sy:*
          13:    gb_un:*
          14:    gb_vi:*
          15:    em_ba:*
          16:    em_fun:*
          17:    em_hum:*
          18:    em_in:*
          19:    em_mu:*
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          25:    em_pl:*
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          27:    em_sts:*

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28:   em_un:*
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30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1110	100.0	1110	6	BD185453	BD185453 Human neu
2	1102	99.3	1110	6	AR216118	AR216118 Sequence
3	1079.4	97.2	1209	6	AR216117	AR216117 Sequence
4	1079.4	97.2	1564	6	E43974	E43974 Novel G pro
5	1079.4	97.2	1564	6	E50810	E50810 Novel G pro
6	1079.4	97.2	1564	6	E50811	E50811 Novel G pro
7	1079.4	97.2	1564	6	AX299473	AX299473 Sequence
8	1079.4	97.2	1564	6	AX299475	AX299475 Sequence
9	1079.4	97.2	1564	6	AX549082	AX549082 Sequence
10	1079.4	97.2	1564	6	AX746121	AX746121 Sequence
11	1079.4	97.2	1564	6	AX840912	AX840912 Sequence
12	1079.4	97.2	1564	9	AF041243	AF041243 Homo sapi
13	1078.4	97.2	1133	6	E43973	E43973 Novel G pro
14	1078.4	97.2	1133	6	AX746120	AX746120 Sequence
15	1078.4	97.2	1170	6	E43972	E43972 Novel G pro
16	1078.4	97.2	1170	6	AX746118	AX746118 Sequence
17	1077.8	97.1	1209	6	BD185452	BD185452 Human neu
18	1075.2	96.9	1116	6	AR216119	AR216119 Sequence
19	1075.2	96.9	1133	6	BD185454	BD185454 Human neu
20	1074.6	96.8	1278	6	AX280925	AX280925 Sequence
21	883.4	79.6	2200	10	AY336083	AY336083 Mus muscu
22	881	79.4	2469	10	AF041244	AF041244 Rattus no
23	688	62.0	843	6	AR109899	AR109899 Sequence
24	661	59.5	789	6	AR109632	AR109632 Sequence
25	661	59.5	789	6	E12154	E12154 cDNA encodi
26	661	59.5	789	6	AR300942	AR300942 Sequence
27	571.8	51.5	781	10	AF394596	AF394596 Mus muscu
28	545.6	49.2	3114	10	AF041246	AF041246 Rattus no
29	521.4	47.0	1545	10	AY336084	AY336084 Mus muscu
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32	511.8	46.1	1843	6	AX549084	AX549084 Sequence
33	511.8	46.1	1843	6	AX840914	AX840914 Sequence

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36	505.4	45.5	1805	4	AF164626	AF164626 Canis fam
37	487.2	43.9	597	10	AY255599	AY255599 Mus muscu
38	322.8	29.1	382	4	AF499612	AF499612 Ovis arie
39	296.2	26.7	637	10	AF394597	AF394597 Mus muscu
40	275.2	24.8	328	4	AB092488	AB092488 Bos tauru
41	261.6	23.6	501	4	AF532967	AF532967 Ovis arie
42	241.2	21.7	344	9	F202078S03	AF202080 Homo sapi
43	241.2	21.7	9785	6	AR178605	AR178605 Sequence
44	241.2	21.7	9785	6	AX088174	AX088174 Sequence
45	241.2	21.7	9785	9	AY062030	AY062030 Homo sapi

ALIGNMENTS

RESULT 1
BD185453
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LOCUS       BD185453                1110 bp    DNA       linear    PAT 17-JUN-2003
DEFINITION  Human neuropeptide receptor.
ACCESSION   BD185453
VERSION     BD185453.1  GI:31877653
KEYWORDS    JP 2002360288-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: JP 2002360288-A 2 17-DEC-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Unidentified
            PN   JP 2002360288-A/2
            PD   17-DEC-2002
            PF   02-MAY-2002 JP 2002130838
            PI   DANIEL R SOPPET,YI LI,CRAIG A ROSEN
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,
            PC   A61P3/06,
            PC   A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC
       A61P25/28,
            PC   A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC
               C12N1/21,
            PC   C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Human neuropeptide receptor
            FH   Key             Location/Qualifiers
            FT   source          1. .1110
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match              100.0%;   Score 1110;   DB 6;   Length 1110;
Best Local Similarity    100.0%;   Pred. No. 2.6e-210;
Matches 1110;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110


RESULT 2
AR216118
LOCUS       AR216118                  1110 bp      DNA        linear      PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6410701.
ACCESSION   AR216118
VERSION     AR216118.1  GI:23314431
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 3 25-JUN-2002;
FEATURES            Location/Qualifiers
     source         1. .1110
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

   Query Match        99.3%;   Score 1102;   DB 6;   Length 1110;
   Best Local Similarity   99.5%;   Fied. No. 1e-208;
   Matches 1105;   Conservative    0;   Mismatches    5;   Indels    0;   Gaps    0;

Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121   TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC   180

Qy      181   CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC   240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181   CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC   240

Qy      241   ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG   300
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      241   ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG   300

Qy      301   CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301   CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG   360

Qy      361   GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361   GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC   420

Qy      421   CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG   480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421   GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG   480

Qy      481   GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481   GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT   540

Qy      541   GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA   600
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db      541   GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA   600

Qy      601   CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT   660
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601   GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT   660

Qy      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC   720

Qy      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC   780

Qy      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC   840

Qy      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG   900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG   900

Qy      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT   960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT   960

Qy      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC   1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
             ||||||||||||||||||||||||||||||
Db      1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 3
AR216117

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LOCUS       AR216117                1209 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6410701.
ACCESSION   AR216117
VERSION     AR216117.1  GI:23314430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 1 25-JUN-2002;
FEATURES            Location/Qualifiers
     source         1. .1209
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN
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   Query Match            97.2%;   Score 1079.4;  DB 6;  Length 1209;
   Best Local Similarity  99.4%;   Pred. No. 3.1e-204;
   Matches 1083;  Conservative    0;  Mismatches   6;  Indels    0;  Gaps    0;
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Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||| |||  |||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1081 CTCAGTGGC 1089


RESULT 4
E43974
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LOCUS           E43974                      1564 bp    DNA      linear    PAT 31-JAN-2002
DEFINITION      Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION       E43974
VERSION         E43974.1  GI:18625173
KEYWORDS        JP 2000106888-A/3.
SOURCE          unidentified
  ORGANISM      unidentified
                unclassified.
REFERENCE       1  (bases 1 to 1564)
  AUTHORS       Bergsma,D.J. and Ellis,C.E.
  TITLE         Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL       Patent: JP 2000106888-A 3 18-APR-2000;
                SMITHKLINE BEECHAM CORP
COMMENT         OS   Unidentified
                PN   JP 2000106888-A/3
                PD   18-APR-2000
                PF   21-JUL-1999 JP 1999206116
                PR   30-APR-1997 US    08/846705
                PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
                PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
                  A61P1/14,
                PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
                A61P13/08,
                PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
                PC   A61P31/04,
                PC   A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,
                PC   A61P43/00,
                PC   C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
                PC   G01N33/577//
                PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
                PC   A61K37/02,
                PC   A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
                CC   Strandedness: Single;
                CC   Topology: Linear;
                FH   Key              Location/Qualifiers
                FT   source           1. .1564
                FT                    /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"
ORIGIN

     Query Match              97.2%;  Score 1079.4;  DB 6;  Length 1564;
     Best Local Similarity    99.4%;  Pred. No. 3e-204;
     Matches 1083;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db    1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

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Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGGC 1089
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Db    1234 CTCAGTGGC 1242
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RESULT 5
E50810

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LOCUS       E50810                    1564 bp    DNA    linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50810
VERSION     E50810.1  GI:13023197
KEYWORDS    JP 2000060578-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 1 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000060578-A/1
            PD   29-FEB-2000
            PF   21-JUL-1999 JP 1999206115
            PR   30-APR-1997 US   08/846704
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
            PC   A61K45/00,
            PC   A61K48/00,A61P3/04,A61P9/00,A61P11/06,A61P13/00,A61P25/00, PC
             A61P25/16,
            PC   A61P25/18,A61P25/20,A61P25/22,A61P31/04,A61P31/10,A61P31/12,
            PC   A61P31/18,
            PC   A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC
             G01N33/53,
            PC   G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key              Location/Qualifiers
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            FT                    /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match         97.2%;  Score 1079.4;  DB 6;  Length 1564;
Best Local Similarity   99.4%;  Pred. No. 3e-204;
Matches 1083;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;
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Qy     1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db   754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db   814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db   874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db   934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    ., 994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db.     1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081  CTCAGTGGC 1089
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Db      1234  CTCAGTGGC 1242
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RESULT 6
E50811

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LOCUS       E50811                  1564 bp    DNA       linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50811
VERSION     E50811.1  GI:13023198
KEYWORDS    JP 2000060578-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 2 29-FEB-2000; .
            SMITHKLINE BEECHAM CORP
COMMENT     OS    Unidentified
            PN    JP 2000060578-A/2
            PD    29-FEB-2000
            PF    21-JUL-1999 JP 1999206115
            PR    30-APR-1997 US    08/846704
            PI    DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC    C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
            PC    A61K45/00,
            PC    A61K48/00,A61P3/04,A61P9/00,A61P11/06,A61P13/00,A61P25/00, PC
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            PC    A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC
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            PC    G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC
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            CC    Topology: Linear;
            FH    Key             Location/Qualifiers
            FT    source          1. .1564
            FT                    /organism='Unidentified'.
FEATURES          Location/Qualifiers
     source       1. .1564
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ORIGIN

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Query Match              97.2%;   Score 1079.4;   DB 6;   Length 1564;
Best Local Similarity    99.4%;   Pred. No. 3e-204;
Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy     1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

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Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db   634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db   754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGGC 1089
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Db    1234 CTCAGTGGC 1242


RESULT 7
AX299473
LOCUS       AX299473                1564 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 1 from Patent EP1154019.
ACCESSION   AX299473
VERSION     AX299473.1  GI:17129230
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 1 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match          97.2%;   Score 1079.4;   DB 6;   Length 1564;
  Best Local Similarity   99.4%;   Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db  214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy  121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db  274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy  181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy  241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy  301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy  361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy  541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy  601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy  661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy  721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db  934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy  841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |.||||||||
Db       1234 CTCAGTGGC 1242


RESULT 8
AX299475
LOCUS       AX299475                1564 bp    DNA        linear   PAT 26-NOV-2001
DEFINITION  Sequence 3 from Patent EP1154019.
ACCESSION   AX299475
VERSION     AX299475.1  GI:17129231
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 3 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match            97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity  99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGCAAGACAGCCAAGATGCTG 900
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Db     994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
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RESULT 9
AX549082

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LOCUS       AX549082                1564 bp    DNA        linear   PAT 26-NOV-2002
DEFINITION  Sequence 367 from Patent WO02061087.
ACCESSION   AX549082
VERSION     AX549082.1  GI:25813851
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 367 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1564
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match          97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity  99.4%;  Pred. No. 3e-204;
  Matches 1083; Conservative    0;  Mismatches    6;  Indels    0; Gaps    0;
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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

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Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
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Db     1234 CTCAGTGGC 1242
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RESULT 10
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LOCUS        AX746121                1564 bp    DNA        linear    PAT 12-JUN-2003
DEFINITION   Sequence 4 from Patent EP1156110.
ACCESSION    AX746121
VERSION      AX746121.1  GI:31744927
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Bergsma,D.J. and Ellis,C.E.
  TITLE      G-protein coupled receptor (HFGAN72Y)
  JOURNAL    Patent: EP 1156110-A 4 21-NOV-2001;
             SMITHKLINE BEECHAM CORPORATION (US)
FEATURES             Location/Qualifiers
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   Query Match          97.2%;  Score 1079.4;  DB 6;  Length 1564;
   Best Local Similarity  99.4%;  Pred. No. 3e-204;
   Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

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Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db   1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy   1081 CTCAGTGGC 1089
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RESULT 11
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DEFINITION Sequence 8 from Patent WO03075945.
ACCESSION   AX840912
VERSION   AX840912.1 GI:39979051
KEYWORDS   .
SOURCE   Homo sapiens (human)

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  Query Match          97.2%;   Score 1079.4;  DB 6;   Length 1564;
  Best Local Similarity  99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy   1081 CTCAGTGGC 1089
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Db   1234 CTCAGTGGC 1242


RESULT 12
AF041243
LOCUS       AF041243                1564 bp    mRNA    linear    PRI 24-FEB-1998
DEFINITION  Homo sapiens orexin receptor-1 mRNA, complete cds.
ACCESSION   AF041243
VERSION     AF041243.1  GI:2897123
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
            Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
            Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A.,
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                    Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A.,
                    Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.
  TITLE   Orexins and orexin receptors: a family of hypothalamic
                    neuropeptides and G protein-coupled receptors that regulate feeding
                    behavior
  JOURNAL   Cell 92 (4), 573-585 (1998)
  MEDLINE   98150861
   PUBMED   9491897
REFERENCE   2 (bases 1 to 1564)
  AUTHORS   Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
                    Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
                    Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A.,
                    Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A.,
                    Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (07-JAN-1998) HHMI/Department of Molecular Genetics,
                    University of Texas Southwestern Medical Center at Dallas, 5323
                    Harry Hines Blvd., Rm. Y5.224, Dallas, TX 75235-9050, USA
FEATURES   Location/Qualifiers
     source   1. .1564
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p33"
     CDS   154. .1431
                     /note="OX1R; G protein-coupled receptor"
                     /codon_start=1
                     /product="orexin receptor-1"
                     /protein_id="AAC39601.1"
                     /db_xref="GI:2897124"
                     /translation="MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQ
                     YEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA
                     SLLVDITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARR
                     ARGSILGIWAVSLAIMVPQAAVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSC
                     FFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEP
                     QPRGRAFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKRVFGMFRQASDRE
                     AVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAFSCCLPGLGPCGSLKAPSPR
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ORIGIN

  Query Match   97.2%; Score 1079.4; DB 9; Length 1564;
  Best Local Similarity   99.4%; Pred. No. 3e-204;
  Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

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Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||| |||  |||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGGC 1089
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Db    1234 CTCAGTGGC 1242
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RESULT 13
E43973

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LOCUS          E43973                    1133 bp    DNA      linear    PAT 31-JAN-2002
DEFINITION     Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION      E43973
VERSION        E43973.1  GI:18625172
KEYWORDS       JP 2000106888-A/2.
SOURCE         unidentified
  ORGANISM     unidentified
               unclassified.
REFERENCE      1  (bases 1 to 1133)
  AUTHORS      Bergsma,D.J. and Ellis,C.E.
  TITLE        Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL      Patent: JP 2000106888-A 2 18-APR-2000;
               SMITHKLINE BEECHAM CORP
COMMENT        OS   Unidentified
               PN   JP 2000106888-A/2
               PD   18-APR-2000
               PF   21-JUL-1999 JP 1999206116
               PR   30-APR-1997 US   08/846705
               PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
               PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
                 A61P1/14,
               PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
               A61P13/08,
               PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
               PC   A61P31/04,
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               PC   A61P43/00,
               PC   C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
               PC   G01N33/577//
               PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
               PC   A61K37/02,
               PC   A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
               CC   Strandedness: Single;
               CC   Topology: Linear;
               FH   Key             Location/Qualifiers
               FT   source          1. .1133
               FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN

     Query Match          97.2%;  Score 1078.4;  DB 6;  Length 1133;
     Best Local Similarity  99.4%;  Pred. No. 4.9e-204;
     Matches 1082;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;
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Qy     1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

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Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

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Qy     1081 CTCAGTGG 1088
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Db     1081 CTCAGTGG 1088


RESULT 14
AX746120
LOCUS       AX746120                1133 bp    DNA        linear    PAT 12-JUN-2003
DEFINITION  Sequence 3 from Patent EP1156110.
ACCESSION   AX746120
VERSION     AX746120.1  GI:31744926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (HFGAN72Y)
  JOURNAL   Patent: EP 1156110-A 3 21-NOV-2001;
            SMITHKLINE BEECHAM CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1133
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                     /note="HGS EST 557082"
ORIGIN

     Query Match          97.2%;  Score 1078.4;  DB 6;   Length 1133;
     Best Local Similarity   99.4%;  Pred. No. 4.9e-204;
     Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy    1081 CTCAGTGG 1088
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Db    1081 CTCAGTGG 1088
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RESULT 15
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LOCUS   E43972   1170 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43972
VERSION   E43972.1 GI:18625171
KEYWORDS   JP 2000106888-A/1.
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1170)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE   Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 1 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT   OS   Unidentified
            PN   JP 2000106888-A/1
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US   08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
              A61P1/14,
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            PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
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            PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
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ORIGIN

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Query Match          97.2%;  Score 1078.4;  DB 6;  Length 1170;
Best Local Similarity  99.4%;  Pred. No. 4.9e-204;
Matches 1082;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

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Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Job time : 4500.38 secs

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:52:46 ; Search time 474.138 Seconds
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Perfect score: 1110
Sequence: 1 atggagccctcagccacccc.........ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                  4: geneseqn2001as:*
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                  10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1110	100.0	1110	4	AAS00492	Aas00492 Human neu
2	1102	99.3	1110	2	AAT42827	Aat42827 Neuropept
3	1079.4	97.2	1209	2	AAT42826	Aat42826 Neuropept
4	1079.4	97.2	1564	2	AAV63468	Aav63468 cDNA enco
5	1079.4	97.2	1564	2	AAV68514	Aav68514 Nucleotid
6	1079.4	97.2	1564	4	AAF32103	Aaf32103 Human HFG
7	1079.4	97.2	1564	6	ABA96021	Aba96021 HGS EST 5

8	1079.4	97.2	1564	6	AAI64173		Aai64173	HFGAN72X
9	1079.4	97.2	1564	6	AAI64172		Aai64172	Human HFG
10	1079.4	97.2	1564	7	ABZ42789		Abz42789	Human ore
11	1078.4	97.2	1133	2	AAV68512		Aav68512	Nucleotid
12	1078.4	97.2	1133	6	ABA96020		Aba96020	HGS EST 5
13	1078.4	97.2	1170	2	AAV68511		Aav68511	Nucleotid
14	1078.4	97.2	1170	6	ABA96019		Aba96019	G-protein
15	1077.8	97.1	1278	4	AAS00491		Aas00491	Human neu
16	1077.8	97.1	1564	4	AAS17464		Aas17464	Human G p
17	1076.8	97.0	1133	4	AAS00493		Aas00493	Human neu
18	1075.2	96.9	1133	2	AAT42828		Aat42828	Neuropept
19	1074.6	96.8	1278	5	ABI98014		Abi98014	Non-endog
20	1031.4	92.9	1278	4	AAD09335		Aad09335	Cynomolgo
21	905	81.5	1281	5	AAC85974		Aac85974	Dog orexi
22	661	59.5	789	2	AAT13909		Aat13909	Rabbit G-
23	661	59.5	789	2	AAT51065		Aat51065	G-protein
24	511.8	46.1	1633	2	AAX29700		Aax29700	Human 7-t
25	511.8	46.1	1843	7	ABZ42790		Abz42790	Human ore
26	507	45.7	1335	4	AAF90300		Aaf90300	Nucleotid
27	507	45.7	1335	5	ABI98015		Abi98015	Non-endog
28	241.2	21.7	344	5	AAF56748		Aaf56748	Human HCR
29	241.2	21.7	9785	5	AAF55159		Aaf55159	Nucleotid
30	241.2	21.7	10453	4	AAS17462		Aas17462	Human G p
31	236	21.3	244	4	AAS17449		Aas17449	Human G p
32	228.4	20.6	331	5	AAF56750		Aaf56750	Human HCR
33	223.8	20.2	227	4	AAS17453		Aas17453	Human G p
34	199	17.9	356	4	AAS17445		Aas17445	Human G p
35	198.6	17.9	452	5	AAF56746		Aaf56746	Human HCR
36	181	16.3	263	5	AAF56747		Aaf56747	Human HCR
37	179	16.1	179	4	AAS17447		Aas17447	Human G p
38	161.6	14.6	1290	3	AAA70507		Aaa70507	Novel hum
39	161.6	14.6	1290	3	AAA70508		Aaa70508	Novel hum
40	161.6	14.6	1290	4	AAH78518		Aah78518	Nucleotid
41	161.6	14.6	1290	4	AAH78519		Aah78519	Nucleotid
42	161.6	14.6	1290	7	ACC49315		Acc49315	Human RFR
43	161.6	14.6	1290	7	ACC49316		Acc49316	Human RFR
44	161.6	14.6	1290	9	ADB76179		Adb76179	Altenativ
45	161.6	14.6	1290	9	ADB76178		Adb76178	Human OT7

ALIGNMENTS

RESULT 1
AAS00492
ID   AAS00492 standard; cDNA; 1110 BP.
XX
AC   AAS00492;
XX
DT   17-MAY-2001 (first entry)
XX
DE   Human neuropeptide receptor splice variant 1 cDNA.
XX
KW   Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW   nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW   cardiovascular disorder; autoimmune disorder; infectious disorder;
KW   eating behaviour disorder; narcolepsy; neurological disease;

KW   narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW   protein co-ordinate data; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT   /*tag= a
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PN   WO200117532-A1.
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PD   15-MAR-2001.
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PF   07-SEP-2000; 2000WO-US024518.
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PR   10-SEP-1999;   99US-00393696.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Soppet DR, Li Y, Rosen CA;
XX
DR   WPI; 2001-183276/18.
DR   P-PSDB; AAU00439.
XX
PT   A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT   useful for preventing, treating or ameliorating obesity, narcolepsy,
PT   neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS   Claim 4; Fig 2; 385pp; English.
XX
CC   The present sequence encodes for human neuropeptide receptor splice
CC   variant 1. Two splice variants (AAU00439-AAU00440) and a possible mutant
CC   (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
CC   described. The neuropeptide receptor shows sequence homology to the
CC   neuropeptide Y receptor. Polypeptides and polynucleotides of the
CC   neuropeptide receptor are useful for diagnosing, preventing, or treating
CC   a pathological condition in a subject related to the central nervous and
CC   peripheral nervous systems (CNS and PNS). The polypeptides and
CC   polynucleotides may be used to treat hyperproliferative, cardiovascular,
CC   autoimmune, nervous system or infectious disorders e.g. cancer, heart
CC   disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
CC   diabetes mellitus. In particular they are useful for preventing, treating
CC   or ameliorating a medical condition in a mammal such as obesity/eating
CC   behaviour disorders, narcolepsy, neurological disease, addiction to
CC   narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
CC   headaches and anxiety disorders. The polynucleotides encoding the
CC   neuropeptide receptor can also be used in gene therapy methods for
CC   treating such diseases
XX
SQ   Sequence 1110 BP; 194 A; 369 C; 300 G; 247 T; 0 U; 0 Other;

        Query Match   100.0%;   Score 1110;   DB 4;   Length 1110;
        Best Local Similarity 100.0%;   Pred. No. 4.6e-253;
        Matches 1110; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110


RESULT 2
AAT42827
ID    AAT42827 standard; cDNA; 1110 BP.
XX
AC    AAT42827;
XX
DT    22-FEB-1997   (first entry)
XX
DE    Neuropeptide receptor splice variant-1 gene.
XX
KW    Human; neuropeptide receptor; splice variant; drug screening;
KW    receptor-agonist; receptor-antagonist; anorectic; antitumour;
KW    anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
KW    sedative; diagnostic; gene therapy; ss.
XX
OS    Homo sapiens.
XX
PN    WO9634877-A1.
XX
PD    07-NOV-1996.
XX
PF    05-MAY-1995;    95WO-US005616.
XX
PR    05-MAY-1995;    95WO-US005616.
XX
PA    (HUMA-) HUMAN GENOME SCI INC.
XX
PI    Soppet DR,   Li Y,   Rosen CA;
XX
DR    WPI; 1996-506094/50.
DR    P-PSDB; AAW06125.
XX
PT    Human neuro-peptide receptor polypeptide(s) - used to identify
PT    antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT    obesity, Alzheimer's disease, epilepsy, etc.
XX
PS    Disclosure; Page 50-51; 77pp; English.
XX
```

CC   The sequence encodes human neuropeptide receptor splice variant-1, which
CC   retains activity corresponding to the mature receptor (encoded by
CC   AAT42826). The receptor gene has been isolated from from a human adult
CC   hypothalamus cDNA library, and is structurally related to the G-protein-
CC   coupled receptor family. The receptor may be used in a drug screening
CC   assay for isolation of receptor-agonists and -antagonists, which may be
CC   used as anorectic, antitumour, anticholesterolemic, neuroprotective,
CC   anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be
CC   used in genetic disease diagnosis or gene therapy. The receptor and its
CC   corresponding antibody may also be used in therapy and diagnosis
XX
SQ   Sequence 1110 BP; 194 A; 364 C; 305 G; 247 T; 0 U; 0 Other;

      Query Match   99.3%;   Score 1102;   DB 2;   Length 1110;
      Best Local Similarity 99.5%;   Pred. No. 3.6e-251;
      Matches 1105; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

```
Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
              ||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110


RESULT 3
AAT42826
ID    AAT42826 standard; cDNA; 1209 BP.
XX
AC    AAT42826;
XX
DT    22-FEB-1997  (first entry)
XX
DE    Neuropeptide receptor gene.
XX
KW    Human; neuropeptide receptor; drug screening; receptor-agonist;
KW    receptor-antagonist; anorectic; antitumour; anticholesterolemic;
KW    neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;
KW    gene therapy; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    primer_bind     complement(1. .18)
FT                    /*tag=  a
```

```
FT                      /note= "Binds primer AAT42829"
FT    misc_difference 151. .153
FT                      /*tag=  b
FT                      /codon= seq:CCA, aa:Ala
FT    primer_bind     complement(1190. .1192)
FT                      /*tag=  c
FT                      /note= "Binds primers AAT42830 and AAT42832"
XX
PN    WO9634877-A1.
XX
PD    07-NOV-1996.
XX
PF    05-MAY-1995;    95WO-US005616.
XX
PR    05-MAY-1995;    95WO-US005616.
XX
PA    (HUMA-) HUMAN GENOME SCI INC.
XX
PI    Soppet DR,  Li Y,  Rosen CA;
XX
DR    WPI; 1996-506094/50.
DR    P-PSDB; AAW06124.
XX
PT    Human neuro-peptide receptor polypeptide(s) - used to identify
PT    antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT    obesity, Alzheimer's disease, epilepsy, etc.
XX
PS    Claim 6; Page 48-49; 77pp; English.
XX
CC    The sequence encodes a human neuropeptide receptor, and has been mapped
CC    to human chromosome 1q31-34. The sequence has been isolated from a human
CC    adult hypothalamus cDNA library, and is structurally related to the G-
CC    protein-coupled receptor family. Splice variants are given in AAT42827-
CC    28. The sequence may be amplified by PCR with e.g. primers AAT42829-34
CC    for expression in a host cell. The recombinant receptor may be used in a
CC    drug screening assay for isolation of receptor-agonists and -antagonists,
CC    which may be used as anorectic, antitumour, anticholesterolemic,
CC    neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC    DNA may also be used in genetic disease diagnosis or gene therapy. The
CC    receptor and its corresponding antibody may also be used in therapy and
CC    diagnosis
XX
SQ    Sequence 1209 BP; 206 A; 402 C; 330 G; 271 T; 0 U; 0 Other;

      Query Match          97.2%;   Score 1079.4;  DB 2;  Length 1209;
      Best Local Similarity  99.4%;   Pred. No. 8.3e-246;
      Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1081 CTCAGTGGC 1089
```

RESULT 4
AAV63468

ID   AAV63468 standard; cDNA; 1564 BP.
XX
AC   AAV63468;
XX
DT   26-JAN-1999 (first entry)
XX
DE   cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.
XX
KW   G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;
KW   bulimia; asthma; Parkinson's disease; acute heart failure;
KW   urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW   benign prostatic hypertrophy; neurological disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   154. .1431
FT   /*tag= a
FT   /product= "HFGAN72X"
XX
PN   EP875566-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308563.
XX
PR   30-APR-1997;   97US-00846704.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ, Ellis CE;
XX
DR   WPI; 1998-555432/48.
DR   P-PSDB; AAW80456.
XX
PT   New human G-protein coupled receptor HFGAN72X polypeptide and
PT   polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT   infection, cancer and Parkinson's disease.
XX
PS   Claim 3; Page 7; 24pp; English.
XX
CC   The present sequence encodes a G-protein coupled receptor (HFGAN72X)
CC   polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC   diagnosing diseases related to over or under expression of HFGAN72X

CC   proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC   probes, or determining HFGAN72X protein or mRNA expression levels.
CC   HFGAN72X polypeptides are also useful for screening for compounds which
CC   affect activity of the protein. Diseases that can be treated with
CC   HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC   asthma, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC   and psychotic and neurological disorders
XX
SQ   Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

    Query Match   97.2%;   Score 1079.4;   DB 2;   Length 1564;
    Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
    Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

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            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy     661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy     721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy     781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy     841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy     901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113

Qy     961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1233

Qy     1081 CTCAGTGGC  1089
            |||||||||
Db     1234 CTCAGTGGC  1242


RESULT 5
AAV68514
ID    AAV68514 standard; cDNA; 1564 BP.
XX
AC    AAV68514;
XX
DT    29-JAN-1999  (first entry)
XX
DE    Nucleotide sequence of a probe HGS EST 554692.
XX
KW    Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;
KW    mutation; probe; agonist; antagonist; activation; inhibition;
KW    gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;
KW    anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW    hypotension; hypertension; urinary retention; osteoporosis;
KW    angina pectoris; myocardial infarction; ulcer; allergies;
KW    psychotic disorder; neurological disorder; gene mapping; ss.
XX
OS    Synthetic.
OS    Homo sapiens.
XX
```

PT   New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT   useful as diagnostic reagents and for prevention and treatment of HIV
PT   infections, cancer, osteoporosis and Parkinson's disease.
XX

PS   Example 1; Page 19-20; 22pp; English.
XX
CC   This is the nucleotide sequence of the probe HGS EST 554692 used in the
CC   method of the invention involving the G-protein coupled receptor,
CC   HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing
CC   susceptibility to diseases by detecting mutations in the HFGAN72Y gene
CC   using probes containing the HFGAN72Y nucleotide sequence, and can
CC   diagnose diseases associated with HFGAN72Y imbalance by determining
CC   HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can
CC   be used in treatment to activate/inhibit HFGAN72Y activity, in addition
CC   to direct administration of antisense sequences to prevent expression, or
CC   HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y
CC   protein. Gene therapy may also be used to affect endogenous HFGAN72Y
CC   polypeptide production. HFGAN72Y antibodies are useful for inducing an
CC   immune response to immunise and prevent diseases, and for isolating
CC   HFGAN72Y clones or purifying the polypeptides by affinity chromatography.
CC   HFGAN72Y polypeptides can be administered directly or as a vaccine to
CC   inoculate against diseases. Diseases diagnosed, prevented or treated
CC   include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,
CC   asthma, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,
CC   and psychotic and neurological disorders. The HFGAN72Y polypeptide is
CC   also useful for mapping the gene to a chromosome, allowing gene
CC   inheritance to be studied through linkage analysis
XX
SQ   Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

     Query Match   97.2%;   Score 1079.4; DB 2;   Length 1564;
     Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
     Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

```
Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||| |||   |||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
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Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1234 CTCAGTGGC 1242
```

RESULT 6
AAF32103
ID   AAF32103 standard; cDNA; 1564 BP.
XX
AC   AAF32103;
XX
DT   10-APR-2001 (first entry)
XX
DE   Human HFGAN72 receptor coding sequence SEQ ID NO: 12.
XX
KW   Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;
KW   truncation mutant; ligand; neurodegenerative disorder; pain;
KW   eating disorder; behaviour disorder; mood disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100787-A2.
XX
PD   04-JAN-2001.
XX
PF   22-JUN-2000; 2000WO-US017251.
XX
PR   25-JUN-1999;   99US-0141156P.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI   Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR   WPI; 2001-071483/08.
XX
PT   Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT   are useful in the treatment of a disease or disorder associated with
PT   pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT   neuropathic pain and back pain.
XX
PS   Disclosure; Fig 6; 101pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC   truncated mutant versions. These, and their agonists and antagonists, are
CC   all useful in the treatment of eating, neurodegenerative, behaviour,
CC   mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC   and acute inflammatory conditions

XX
SQ   Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

        Query Match   97.2%;   Score 1079.4; DB 4;   Length 1564;
        Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
        Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            |||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1234 CTCAGTGGC 1242


RESULT 7
ABA96021
ID   ABA96021 standard; cDNA; 1564 BP.
XX
AC   ABA96021;
XX
DT   12-MAR-2002  (first entry)
XX
DE   HGS EST 554692.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation; EST;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW   HGS EST 554692; expressed sequence tag; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;  97US-00846705.
PR   27-OCT-1997;  97EP-00308554.
XX
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PT   New polynucleotide encoding a G-protein coupled receptor designated
PT   HFGAN72Y is useful to diagnose and treat associated diseases including
PT   cancer, infection, cardiac disease and psychotic and neurological
PT   disorders.
XX
PS   Example 1; Page 19-20; 22pp; English.
XX
CC   The sequence represents HGS EST 554692. The sequence was used in the
CC   invention as a probe to screen a human genomic placenta phage library.
CC   The invention relates to a novel isolated polynucleotide encoding
CC   HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,
CC   cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti
CC   -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
CC   polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
CC   subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
CC   antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
CC   expression is used to treat a subject in need of decreased HFGAN72Y
CC   activity or expression. HFGAN72Y-associated diseases include infections,
CC   particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's
CC   disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,
CC   allergies, benign prostatic hypertrophy, and psychotic and neurological
CC   disorders including anxiety, schizophrenia, manic depression, delirium,
CC   dementia, severe mental retardation and dyskinesias such as Huntington's
CC   disease and Tourette's syndrome
XX
SQ   Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

    Query Match   97.2%;   Score 1079.4; DB 6;   Length 1564;
    Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
    Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

```
Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          ||||||||| |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy   1081 CTCAGTGGC 1089
          |||||||||
Db   1234 CTCAGTGGC 1242
```

ID   AAI64173 standard; cDNA; 1564 BP.
XX

AC   AAI64173;
XX

DT   22-JAN-2002 (first entry)
XX

DE   HFGAN72X G coupled receptor polypeptide partial sequence.
XX

KW   Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW   cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW   antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW   osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW   Parkinson's disease; acute heart failure; hypotension; hypertension;
KW   urinary retention; osteoporosis; angina pectoris; probe;
KW   myocardial infarction; ulcers; asthma; allergy; delirium; dementia;
KW   benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW   dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX

OS   Homo sapiens.
XX

FH   Key   Location/Qualifiers
FT   CDS   154. .1362
FT   /*tag= a
FT   /partial
FT   /product= "HFGAN72X protein"
FT   /note= "The specification states that this is a partial
FT   sequence even though it contains start and stop codons;
FT   HFGAN72X is a G coupled receptor polypeptide"
FT   /transl_except= (pos:991. .993, aa:Ala)
XX

PN   EP1154019-A2.
XX

PD   14-NOV-2001.
XX

PF   27-OCT-1997; 2001EP-00203008.
XX

PR   30-APR-1997; 97US-00846704.
PR   27-OCT-1997; 97EP-00308563.
XX

PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX

PI   Bergsma DJ, Ellis CE;
XX

DR   WPI; 2002-012659/02.
DR   P-PSDB; AAG78346.
XX

PT   Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT   treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT   disease, and acute heart failure.
XX

PS   Example 3; Page 9; 24pp; English.
XX

CC   The present sequence is that of a known partial nucleotide sequence
CC   encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify
CC   the HFGAN72X gene (AAI64173). The specification describes a newly

```
CC    isolated polynucleotide encoding a human HFGAN72X G coupled receptor
CC    polypeptide. The protein of the invention has antibacterial, fungicide,
CC    virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,
CC    nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,
CC    neuroleptic, antidepressant, anticonvulsant and osteopathic activities.
CC    HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to
CC    treat diseases requiring increased activity or expression of HFGAN72X;
CC    for recombinant production of HFGAN72X; diagnose diseases by detecting
CC    mutations in genomic sequences and in chromosome identification and
CC    mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC    therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC    purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC    PNs are used to identify (ant)agonists of HFGAN72X, useful
CC    therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC    polypeptides that compete with ligands for binding to HFGAN72X proteins
CC    are also useful therapeutically and diagnostically. HFGAN72X-related
CC    diseases include infections (bacterial, viral, fungal or protozoal,
CC    particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC    disease; acute heart failure; hypotension; hypertension; urinary
CC    retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC    asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC    manic depression; delirium; dementia; severe mental retardation and
CC    dyskinesias
XX
SQ    Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

    Query Match            97.2%;  Score 1079.4;  DB 6;  Length 1564;
    Best Local Similarity  99.4%;  Pred. No. 8.9e-246;
    Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
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Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||   |||  ||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1234 CTCAGTGGC 1242
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RESULT 9
AAI64172
ID   AAI64172 standard; cDNA; 1564 BP.
XX
AC   AAI64172;
XX
DT   22-JAN-2002 (first entry)

CC   The present sequence is that of a cDNA encoding a HFGAN72X polypeptide
CC   (AAG78345). The specification describes a newly isolated polynucleotide
CC   encoding a HFGAN72X G coupled receptor polypeptide. The protein of the
CC   invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,
CC   cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,
CC   antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant
CC   and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to
CC   express HFGAN72X in vivo, to treat diseases requiring increased activity
CC   or expression of HFGAN72X; for recombinant production of HFGAN72X;
CC   diagnose diseases (or susceptibility to them) by detecting mutations in
CC   genomic sequences and in chromosome identification and mapping. HFGAN72X
CC   polypeptides are used to raise specific antibodies; as therapeutic agents
CC   ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X
CC   proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to

CC   identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids
CC   that inhibit expression of HFGAN72X and polypeptides that compete with
CC   ligands for binding to HFGAN72X proteins are also useful therapeutically
CC   and diagnostically. HFGAN72X-related diseases include infections
CC   (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;
CC   cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;
CC   hypotension; hypertension; urinary retention; osteoporosis; angina
CC   pectoris; myocardial infarction; ulcers; asthma; allergy; benign
CC   prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium
CC   ; dementia; severe mental retardation and dyskinesias
XX
SQ   Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

        Query Match   97.2%;   Score 1079.4;   DB 6;   Length 1564;
        Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
        Matches 1083;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

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Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||  |||||||||||||||||||||||||||||||||||||||||||||||||·|||||
Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             |||·||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
             ||||||||·|||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             |||·||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||·||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081 CTCAGTGGC 1089
             |||||||||
Db      1234 CTCAGTGGC 1242
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RESULT 10
ABZ42789
ID   ABZ42789 standard; DNA; 1564 BP.
XX
AC   ABZ42789;
XX
DT   04-MAR-2003 (first entry)
XX
DE   Human orexin receptor 1 nucleotide SEQ ID NO:367.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,   Roush CL,   Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81941.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

       Query Match   97.2%;   Score 1079.4;   DB 7;   Length 1564;
       Best Local Similarity   99.4%;   Pred. No. 8.9e-246;
       Matches 1083;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

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Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     514 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           | | | | | | | | |   | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
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Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
            |||||||||
Db     1234 CTCAGTGGC 1242


RESULT 11
AAV68512
ID      AAV68512 standard; cDNA; 1133 BP.
XX
AC      AAV68512;
XX
DT      29-JAN-1999  (first entry)
XX
DE      Nucleotide sequence of HGS EST 557082.
XX
KW      HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;
KW      probe; agonist; antagonist; activation; inhibition; gene therapy;
KW      antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;
KW      bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;
KW      hypertension; urinary retention; osteoporosis; angina pectoris;
KW      myocardial infarction; ulcer; allergies; psychotic disorder;
KW      neurological disorder; gene mapping; ss.
XX
OS      Homo sapiens.
XX
PN      EP875565-A2.
XX
PD      04-NOV-1998.
XX
PF      27-OCT-1997;   97EP-00308554.
XX
PR      30-APR-1997;   97US-00846705.
XX
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI      Bergsma DJ,  Ellis C;
XX
DR      WPI; 1998-570286/49.
XX
PT      New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT      useful as diagnostic reagents and for prevention and treatment of HIV
```

PT   infections, cancer, osteoporosis and Parkinson's disease.
XX
PS   Example 1; Page 18-19; 22pp; English.
XX
CC   This is the nucleotide sequence of the HGS EST 557082 used in the method
CC   of the invention involving the G-protein coupled receptor, HFGAN72Y. Its
CC   polypeptides and polynucleotides are useful for diagnosing susceptibility
CC   to diseases by detecting mutations in the HFGAN72Y gene using probes
CC   containing the HFGAN72Y nucleotide sequence, and can diagnose diseases
CC   associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or
CC   mRNA expression levels. Agonists/antagonists can be used in treatment to
CC   activate/inhibit HFGAN72Y activity, in addition to direct administration
CC   of antisense sequences to prevent expression, or HFGAN72Y polypeptides to
CC   treat conditions associated with a lack HFGAN72Y protein. Gene therapy
CC   may also be used to affect endogenous HFGAN72Y polypeptide production.
CC   HFGAN72Y antibodies are useful for inducing an immune response to
CC   immunise and prevent diseases, and for isolating HFGAN72Y clones or
CC   purifying the polypeptides by affinity chromatography. HFGAN72Y
CC   polypeptides can be administered directly or as a vaccine to inoculate
CC   against diseases. Diseases diagnosed, prevented or treated include HIV-1
CC   or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   ulcers; allergies, benign prostatic hypertrophy, and psychotic and
CC   neurological disorders. The HFGAN72Y polypeptide is also useful for
CC   mapping the gene to a chromosome, allowing gene inheritance to be studied
CC   through linkage analysis
XX
SQ   Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

    Query Match   97.2%;   Score 1078.4;   DB 2;   Length 1133;
    Best Local Similarity   99.4%;   Pred. No. 1.4e-245;
    Matches 1082;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

```
Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGG 1088
            ||||||||
Db     1081 CTCAGTGG 1088


RESULT 12
ABA96020
ID   ABA96020 standard; cDNA; 1133 BP.
```

SQ   Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

    Query Match   97.2%;   Score 1078.4;   DB 6;   Length 1133;
    Best Local Similarity 99.4%;   Pred. No. 1.4e-245;
    Matches 1082; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||.||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           ||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

```
Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
```

RESULT 13
AAV68511
ID   AAV68511 standard; cDNA; 1170 BP.
XX
AC   AAV68511;
XX
DT   29-JAN-1999 (first entry)
XX
DE   Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.
XX
KW   G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;
KW   antagonist; activation; inhibition; gene therapy; antibody;
KW   immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;
KW   asthma; Parkinson's disease; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; angina pectoris;
KW   myocardial infarction; ulcer; allergies; psychotic disorder;
KW   neurological disorder; gene mapping; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .1170
FT   /*tag= a
FT   /product= "HFGAN72Y protein"
XX
PN   EP875565-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308554.
XX

CC   This is the nucleotide sequence of the G-protein coupled receptor,
CC   HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC   polynucleotides are useful for diagnosing susceptibility to diseases by
CC   detecting mutations in the HFGAN72Y gene using probes containing the
CC   HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC   HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC   levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC   HFGAN72Y activity, in addition to direct administration of antisense
CC   sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC   conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC   be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC   antibodies are useful for inducing an immune response to immunise and
CC   prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC   polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC   administered directly or as a vaccine to inoculate against diseases.
CC   Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC   infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC   disease, acute heart failure, hypotension, hypertension, urinary
CC   retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC   allergies, benign prostatic hypertrophy, and psychotic and neurological
CC   disorders. The HFGAN72Y polypeptide is also useful for mapping the gene
CC   to a chromosome, allowing gene inheritance to be studied through linkage
CC   analysis
XX
SQ   Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

      Query Match   97.2%;   Score 1078.4;   DB 2;   Length 1170;
      Best Local Similarity   99.4%;   Pred. No. 1.4e-245;
      Matches 1082; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

```
Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||  |||  |||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
             | | | | | | | |
Db      1081 CTCAGTGG 1088
```

RESULT 14
ABA96019
ID   ABA96019 standard; cDNA; 1170 BP.
XX
AC   ABA96019;
XX
DT   12-MAR-2002   (first entry)
XX
DE   G-protein coupled receptor (HFGAN72Y) cDNA.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .1170
FT   /*tag= a
FT   /product= "HGFAN72Y"
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;   97US-00846705.
PR   27-OCT-1997;   97EP-00308554.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ, Ellis CE;
XX
DR   WPI; 2002-084320/12.
DR   P-PSDB; ABB08208.
XX
PT   New polynucleotide encoding a G-protein coupled receptor designated
PT   HFGAN72Y is useful to diagnose and treat associated diseases including
PT   cancer, infection, cardiac disease and psychotic and neurological
PT   disorders.
XX
PS   Claim 3; Page 7; 22pp; English.
XX
CC   The sequence encodes G-protein coupled receptor HFGAN72Y. The invention

CC   relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide.
CC   The polypeptide of the invention has cytostatic, cardiant, analgesic,
CC   tranquillising, nootropic, neuroprotective, and anti-asthmatic activity.
CC   The HFGAN72Y has a use in gene therapy. The HFGAN72Y polynucleotide or an
CC   HFGAN72Y polypeptide agonist are used to treat a subject in need of
CC   enhanced HFGAN72Y activity or expression. An HFGAN72Y antagonist or
CC   competitor, or nucleic acid which inhibits HFGAN72Y expression is used to
CC   treat a subject in need of decreased HFGAN72Y activity or expression.
CC   HFGAN72Y-associated diseases include infections, particularly by HIV-1 or
CC   HIV-2, pain, anorexia, bulimia, Parkinson's disease, cardiac diseases,
CC   cancers, ulcers, urinary retention, asthma, allergies, benign prostatic
CC   hypertrophy, and psychotic and neurological disorders including anxiety,
CC   schizophrenia, manic depression, delirium, dementia, severe mental
CC   retardation and dyskinesias such as Huntington's disease and Tourette's
CC   syndrome
XX
SQ   Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

    Query Match   97.2%;   Score 1078.4;   DB 6;   Length 1170;
    Best Local Similarity   99.4%;   Pred. No. 1.4e-245;
    Matches 1082; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy    541 .GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy   1081 CTCAGTGG 1088
          ||||||||
Db   1081 CTCAGTGG 1088
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RESULT 15
AAS00491
ID   AAS00491 standard; cDNA; 1278 BP.
XX
AC   AAS00491;
XX
DT   17-MAY-2001 (first entry)
XX
DE   Human neuropeptide receptor cDNA.
XX
KW   Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW   nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW   cardiovascular disorder; autoimmune disorder; infectious disorder;
KW   eating behaviour disorder; narcolepsy; neurological disease;
KW   narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;

KW   protein co-ordinate data; chromosome 1; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .1278
FT   /*tag= a
FT   /product= "neuropeptide receptor"
XX
PN   WO200117532-A1.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024518.
XX
PR   10-SEP-1999;   99US-00393696.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Soppet DR, Li Y, Rosen CA;
XX
DR   WPI; 2001-183276/18.
DR   P-PSDB; AAU00438.
XX
PT   A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT   useful for preventing, treating or ameliorating obesity, narcolepsy,
PT   neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS   Claim 4; Fig 1; 385pp; English.
XX
CC   The present sequence encodes for a novel human neuropeptide receptor
CC   which shows sequence homology to the neuropeptide Y receptor. Two splice
CC   variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
CC   mutant (AAU00442) are also described. Polypeptides and polynucleotides of
CC   the neuropeptide receptor are useful for diagnosing, preventing, or
CC   treating a pathological condition in a subject related to the central
CC   nervous and peripheral nervous systems (CNS and PNS). The polypeptides
CC   and polynucleotides may be used to treat hyperproliferative,
CC   cardiovascular, autoimmune, nervous system or infectious disorders e.g.
CC   cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV
CC   infection and diabetes mellitus. In particular they are useful for
CC   preventing, treating or ameliorating a medical condition in a mammal such
CC   as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC   addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC   migraine headaches and anxiety disorders. The polynucleotides encoding
CC   the neuropeptide receptor can also be used in gene therapy methods for
CC   treating such diseases
XX
SQ   Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

    Query Match   97.1%; Score 1077.8; DB 4; Length 1278;
    Best Local Similarity 99.4%; Pred. No. 2e-245;
    Matches 1082; Conservative   0; Mismatches, 7; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy    61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG  120
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Qy   121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC  180
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Db   121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC  180

Qy   181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  240
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Db   181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  240

Qy   241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300
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Db   241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300

Qy   301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360
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Db   301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360

Qy   361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420
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Db   361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420

Qy   421  CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
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Db   421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480

Qy   481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
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Qy   541  GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
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Db   541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy   601  CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
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Db   601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

Qy   661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
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Db   661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy   721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
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Db   721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780

Qy   781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC  840

Qy   841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
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Db   841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
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Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy     1081 CTCAGTGGC 1089
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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       Pred. No. is the number of results predicted by chance to have a
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                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1110	100.0	1110	5	PCT-US95-05616-3	Sequence 3, Appli
2	1102	99.3	1110	4	US-08-462-509B-3	Sequence 3, Appli
3	1079.4	97.2	1209	4	US-08-462-509B-1	Sequence 1, Appli
4	1079.4	97.2	1564	2	US-08-846-705-4	Sequence 4, Appli
5	1079.4	97.2	1564	3	US-08-846-704-1	Sequence 1, Appli
6	1079.4	97.2	1564	3	US-08-846-704-3	Sequence 3, Appli
7	1078.4	97.2	1133	2	US-08-846-705-3	Sequence 3, Appli
8	1078.4	97.2	1170	2	US-08-846-705-1	Sequence 1, Appli
9	1077.8	97.1	1209	5	PCT-US95-05616-1	Sequence 1, Appli
10	1075.2	96.9	1116	4	US-08-462-509B-5	Sequence 5, Appli
11	1075.2	96.9	1133	5	PCT-US95-05616-5	Sequence 5, Appli

12	688	62.0	843	3	US-08-513-974B-375	Sequence 375, App
13	661	59.5	789	3	US-08-513-974B-55	Sequence 55, Appl
14	661	59.5	789	4	US-09-461-436B-55	Sequence 55, Appl
15	511.8	46.1	1633	3	US-09-119-788-1	Sequence 1, Appli
16	241.2	21.7	9785	4	US-09-479-128-1	Sequence 1, Appli
17	161.6	14.6	1293	3	US-09-255-368-7	Sequence 7, Appli
18	154.6	13.9	1410	3	US-09-255-368-1	Sequence 1, Appli
19	120.4	10.8	168575	4	US-09-426-290-1	Sequence 1, Appli
20	117.4	10.6	1110	3	US-08-513-974B-31	Sequence 31, Appl
21	117.4	10.6	1110	3	US-08-776-971-26	Sequence 26, Appl
22	117.4	10.6	1110	4	US-09-461-436B-31	Sequence 31, Appl
23	117.4	10.6	1331	3	US-08-513-974B-322	Sequence 322, App
24	117.4	10.6	1331	3	US-08-776-971-103	Sequence 103, App
25	108.8	9.8	1113	3	US-09-172-353-1	Sequence 1, Appli
26	108.8	9.8	1113	4	US-09-799-955-1	Sequence 1, Appli
27	107.2	9.7	669	3	US-08-513-974B-314	Sequence 314, App
28	107.2	9.7	669	3	US-08-776-971-99	Sequence 99, Appl
29	101.6	9.2	1110	4	US-09-170-496D-25	Sequence 25, Appl
30	101.6	9.2	1110	4	US-09-170-496D-177	Sequence 177, App
31	101.6	9.2	1344	4	US-09-016-434-1295	Sequence 1295, Ap
32	101.6	9.2	1356	1	US-07-978-892A-4	Sequence 4, Appli
33	101.6	9.2	1535	4	US-09-016-434-1051	Sequence 1051, Ap
34	101.6	9.2	1969	1	US-07-937-609-28	Sequence 28, Appl
35	101.6	9.2	1969	3	US-08-029-170-28	Sequence 28, Appl
36	98.4	8.9	1621	1	US-08-722-001-13	Sequence 13, Appl
37	98.4	8.9	1776	1	US-08-722-001-29	Sequence 29, Appl
38	98.4	8.9	2002	4	US-09-016-434-1172	Sequence 1172, Ap
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43	98.4	8.9	2140	2	US-08-722-190-1	Sequence 1, Appli
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45	98.4	8.9	2140	3	US-09-206-899-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
PCT-US95-05616-3
; Sequence 3, Application PC/TUS9505616
;   GENERAL INFORMATION:
;   APPLICANT: LI, ET AL.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;   ADDRESSEE: CECCHI, STEWART & OLSTEIN
;   STREET: 6 BECKER FARM ROAD
;   CITY: ROSELAND
;   STATE: NEW JERSEY
;   COUNTRY: USA
;   ZIP: 07068
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: IBM PS/2

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   Query Match               100.0%;   Score 1110;   DB 5;   Length 1110;
   Best Local Similarity    100.0%;   Pred. No. 4.1e-255;
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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||.|||||||||
Db    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy    1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
           ||||||||||||||||||||||||||||||
Db    1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 2
US-08-462-509B-3
; Sequence 3, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue

```
;        CITY:  Rockiville
;        STATE:  MD
;        COUNTRY:  USA
;        ZIP:  20850
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/462,509B
;        FILING DATE:  05-JUN-1995
;        CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  WO PCT/US95/05616
;        FILING DATE:  05-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  Wales, Michele M.
;        REGISTRATION NUMBER:  43,975
;        REFERENCE/DOCKET NUMBER:  PF168P1
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  301-309-8504
;        TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  1110 base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;        NAME/KEY:  CDS
;        LOCATION:  1..1110
US-08-462-509B-3


   Query Match              99.3%;  Score 1102;  DB 4;  Length 1110;
   Best Local Similarity    99.5%;  Pred. No. 3.3e-253;
   Matches 1105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300

Qy     301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360

Qy     361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420

Qy     421  CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480

Qy     481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540

Qy     541  GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
            |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy     601  CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
            |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

Qy     661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy     721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780

Qy     781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840

Qy     841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900

Qy     901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960

Qy     961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080

Qy     1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA  1110
            ||||||||||||||||||||||||||||||
Db     1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA  1110
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RESULT 3
US-08-462-509B-1
; Sequence 1, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockiville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1209
US-08-462-509B-1

    Query Match   97.2%; Score 1079.4; DB 4; Length 1209;
    Best Local Similarity 99.4%; Pred. No. 8.1e-248;
    Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

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                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                  ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                  ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
                  ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1081 CTCAGTGGC 1089
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RESULT 4
US-08-846-705-4
; Sequence 4, Application US/08846705
; Patent No. 5935814
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/846,705
;   FILING DATE: 30-APR-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: PRESTIA, PAUL F
;   REGISTRATION NUMBER: 23,031
;   REFERENCE/DOCKET NUMBER: GH-70003
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 610-407-0700
;   TELEFAX: 610-407-0701
;   TELEX: 846169
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1564 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

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     Query Match              97.2%;  Score 1079.4;  DB 2;  Length 1564;
     Best Local Similarity    99.4%;  Pred. No. 8.7e-248;
     Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
               ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db       1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081  CTCAGTGGC 1089
               |||||||||
Db       1234  CTCAGTGGC 1242
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RESULT 5
US-08-846-704-1
; Sequence 1, Application US/08846704
; Patent No. 6020157
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E.
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/846,704
;   FILING DATE: 30-APR-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: PRESTIA, PAUL F

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   Query Match              97.2%;   Score 1079.4;   DB 3;   Length 1564;
   Best Local Similarity    99.4%;   Pred. No. 8.7e-248;
   Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
             |||||||||  ||||    |||||||||||||||||||||||||||||||||||||||||||
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Db       694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  753

Qy       601  CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy       661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy       721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy       781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy       841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy       901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113

Qy       961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1173

Qy      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1233

Qy      1081  CTCAGTGGC  1089
              |||||||||
Db      1234  CTCAGTGGC  1242
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RESULT 6
US-08-846-704-3
; Sequence 3, Application US/08846704
; Patent No. 6020157
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E.
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette

Query Match   97.2%;   Score 1079.4;   DB 3;   Length 1564;
Best Local Similarity   99.4%;   Pred. No. 8.7e-248;
Matches 1083;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGC 1089
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Db     1234 CTCAGTGGC 1242
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RESULT 7
US-08-846-705-3
; Sequence 3, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.

```
;     APPLICANT:  ELLIS, CATHERINE E
;     TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;     NUMBER OF SEQUENCES:  5
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  RATNER & PRESTIA
;       STREET:  P.O. BOX 980
;       CITY:  VALLEY FORGE
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19482
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/846,705
;       FILING DATE:  30-APR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1133 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-705-3
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   Query Match              97.2%;  Score 1078.4;  DB 2;  Length 1133;
   Best Local Similarity    99.4%;  Pred. No. 1.4e-247;
   Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
             |||||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy          1081 CTCAGTGG 1088
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Db          1081 CTCAGTGG 1088


RESULT 8
US-08-846-705-1
; Sequence 1, Application US/08846705
; Patent No. 5935814
;   GENERAL INFORMATION:
;     APPLICANT:  BERGSMA, DERK J.
;     APPLICANT:  ELLIS, CATHERINE E
;     TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;     NUMBER OF SEQUENCES:  5
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  RATNER & PRESTIA
;       STREET:  P.O. BOX 980
;       CITY:  VALLEY FORGE
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19482
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/846,705
;       FILING DATE:  30-APR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1170 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-705-1

    Query Match            97.2%;  Score 1078.4;  DB 2;  Length 1170;
    Best Local Similarity  99.4%;  Pred. No. 1.4e-247;
    Matches 1082;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy           1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           ||||||||| |||    |||||||||||||||||||||||||||||||||||||||||||
Db     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGG 1088
            ||||||||
Db     1081 CTCAGTGG 1088
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RESULT 9
PCT-US95-05616-1
; Sequence 1, Application PC/TUS9505616
;   GENERAL INFORMATION:
;     APPLICANT:  LI, ET AL.
;     TITLE OF INVENTION:  Human Neuropeptide Receptor
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;       ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;       STREET:  6 BECKER FARM ROAD
;       CITY:  ROSELAND
;       STATE:  NEW JERSEY
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 INCH DISKETTE
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/05616
;       FILING DATE:  concurrently
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-268
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1209 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
PCT-US95-05616-1
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Query Match               97.1%;   Score 1077.8;   DB 5;   Length 1209;
Best Local Similarity     99.4%;   Pred. No. 1.9e-247;
Matches 1082;   Conservative    0;   Mismatches    7;   Indels    0;   Gaps    0;


Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480


Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540


Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600


Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660


Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720


Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081  CTCAGTGGC 1089
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Db   1081  CTCAGTGGC 1089
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RESULT 10
US-08-462-509B-5
; Sequence 5, Application US/08462509B
; Patent No. 6410701
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockiville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/462,509B
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US95/05616
;   FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1
;   TELECOMMUNICATION INFORMATION:

Query Match   96.9%; Score 1075.2; DB 4; Length 1116;
Best Local Similarity   99.3%; Pred. No. 7.9e-247;
Matches 1080; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy     421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy     541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
             ||||||||
Db      1081 CTCAGTGG 1088
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RESULT 11
PCT-US95-05616-5
; Sequence 5, Application PC/TUS9505616
;   GENERAL INFORMATION:
;   APPLICANT: LI, ET AL.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;   ADDRESSEE: CECCHI, STEWART & OLSTEIN
;   STREET: 6 BECKER FARM ROAD
;   CITY: ROSELAND
;   STATE: NEW JERSEY
;   COUNTRY: USA
;   ZIP: 07068
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: MS-DOS

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;     SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/05616
;       FILING DATE:  concurrently
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-268
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1133 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
PCT-US95-05616-5
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   Query Match              96.9%;  Score 1075.2;  DB 5;  Length 1133;
   Best Local Similarity    99.3%;  Pred. No. 7.9e-247;
   Matches 1080;  Conservative     0;  Mismatches     8;  Indels     0;  Gaps     0;
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Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy    481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
           ||||||||||||||||||||||||||||||||-||||||||||||||||||||||||||||
Db    481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540

Qy    541  GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
           |||||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||
Db    541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy    601  CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
           |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

Qy    661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy    721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780

Qy    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840

Qy    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900

Qy    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960

Qy    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080

Qy    1081 CTCAGTGG  1088
           ||||||||
Db    1081 CTCAGTGG  1088
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RESULT 12
US-08-513-974B-375
; Sequence 375, Application US/08513974B
; Patent No. 6114139
;   GENERAL INFORMATION:
;   APPLICANT: Hinuma, Shuji
;   APPLICANT: Hosoya, Masaki
;   APPLICANT: Fujii, Ryo
;   APPLICANT: Ohtaki, Tetsuya
;   APPLICANT: Fukusumi, Shoji
;   APPLICANT: Ohgi, Kazuhiro
;   TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

```
;     TITLE OF INVENTION:   PRODUCTION, AND USE THEREOF
;     NUMBER OF SEQUENCES:   380
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
```

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   Query Match              62.0%;   Score 688;   DB 3;   Length 843;
   Best Local Similarity    89.2%;   Pred. No. 1e-154;
   Matches  742;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;


Qy       252 CATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCT 311
                 |  |   ||| |||||| ||||| || || ||||||||| || ||||||||||||||||| ||
Db         9 CGTGTTCATCCTGTCACTGGCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCT 68


Qy       312 GCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
             |||||| |||||||| || |||||||| || |||||||||||||||||||||||||||||
Db        69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128


Qy       372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCG 431
             |||||||||| ||||||||||||||||| |||||| ||||||||| ||||| |||||||||
Db       129 TCTACAGGCCGTGTCCGTGTCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188


Qy       432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTC 491
             |||||| |||||||||||||||| || ||||||||||||||| ||||||||| ||||| |||||
Db       189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTC 248


Qy       492 CATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCA 551
             |||||| |||||||||||| |||||||||| |||||||||| ||||||||| |||||| |
Db       249 CATCCTCGGCATCTGGGCGGTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGA 308


Qy       552 ATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGA 611
              |    ||||| ||||||||| |||||| |||||||||| || ||| | || ||||| ||||
Db       309 GTGTAGCAGCGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368


Qy      . 612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTA 671
              |||||||||| ||||| || ||||||||||||||||||| |||||| ||||||||||||
Db       369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTA 428


Qy       672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||
Db       429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488


Qy       732 CCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCA 791
             ||||||||||||||||||||||||| || |||||||| |||||||||| ||||||||||
Db       489 CCGCCAGATCCCCGGCACCACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCA 548


Qy       792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCT 851
             |||||  |||| || || ||||||||||  |||||||||||||||||||| ||||||||||
Db       549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCT 608
```

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Qy    852 GGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT 911
          ||| || |||||| |||||||| || ||||||||||| |||||||||||||||||||||| |||
Db    609 GGCCGAGGTGAAACAGATGCGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT 668


Qy    912 GCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTT 971
          |||||||||||||||||||||||||| |||||||| |||||||| ||||| ||||||||| ||
Db    669 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTT 728


Qy    972 CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCA 1031
          |||||||||||||||||||||| ||||| || || |||||||||||||||||||||||||||
Db    729 CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCA 788


Qy   1032 CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTC 1083
          |||||||||||||||||||||| ||||| ||| || ||||| |||||||
Db    789 CTGGCTGGTGTACGCCAACAGCGCCGCCAATCCCCTCCTCTACTCCTTCCTC 840



RESULT 13
US-08-513-974B-55
; Sequence 55, Application US/08513974B
; Patent No. 6114139
;   GENERAL INFORMATION:
;     APPLICANT:  Hinuma, Shuji
;     APPLICANT:  Hosoya, Masaki
;     APPLICANT:  Fujii, Ryo
;     APPLICANT:  Ohtaki, Tetsuya
;     APPLICANT:  Fukusumi, Shoji
;     APPLICANT:  Ohgi, Kazuhiro
;     TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;     TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;     NUMBER OF SEQUENCES:  380
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
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US-08-513-974B-55

  Query Match   59.5%;   Score 661; DB 3; Length 789;
  Best Local Similarity 89.9%;   Pred. No. 2.6e-148;
  Matches 709; Conservative   0; Mismatches   80; Indels   0; Gaps   0;

Qy   271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
                || || || |||||||| || ||||||||||||||| |||||||| |||||||| ||
Db   1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy'   331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
                |||||||| || |||||||||||||||||||||||||||||||||||||| ||||||||||
Db   61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy   391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
                ||||||| ||||| |||||||||| |||| ||||||||||||||| ||||||||||||
Db   121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy   451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
                || || |||||||||||| |||||||| ||||| |||||||||| |||||||||||

```
Db      181  CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG  240

Qy      511  GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCT  570
             ||||||||||| ||||||||||| |||||||| |||||| | |  ||||| ||||||||
Db      241  GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC  300

Qy      571  GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC  630
             ||||| ||||||||||| || ||| | ||  ||||| |||| ||||||||||| |||||
Db      301  GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG  360

Qy      631  TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC  690
             || |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db      361  TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC  420

Qy      691  ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC  750
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      421  ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC  480

Qy      751  ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGGACCTGGAGCAG  810
             ||||| || |||||||| ||||||||||| ||||||||||||||||| |||| ||  |||
Db      481  ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG  540

Qy      811  GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG  870
             ||||||||    |||||||||||||||||||| |||||||||||| || ||||| ||||||
Db      541  GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG  600

Qy      871  CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC  930
             || || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      601  CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC  660

Qy      931  TACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC  990
             ||||| ||||||||| ||||||||| ||||| |||||||| |||||||||||||||||||
Db      661  TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC  720

Qy      991  AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC  1050
             || ||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db      721  AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC  780

Qy     1051  AGCGCTGCC  1059
             ||||| |||
Db      781  AGCGCCGCC  789
```

RESULT 14
US-09-461-436B-55
; Sequence 55, Application US/09461436B
; Patent No. 6538107
;   GENERAL INFORMATION:
;   APPLICANT: Shuji Hinuma
;   Yasuaki Ito
;   Ryo Fujii
;   TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;   Production, And Use Thereof
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Edwards & Angell, LLP
;   STREET: 101 Federal Street

    Query Match   59.5%; Score 661; DB 4; Length 789;
    Best Local Similarity   89.9%; Pred. No. 2.6e-148;

Matches 709; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

```
Qy    271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
          || || || |||||||| || |||||||||||||||| |||||||| |||||||| ||
Db      1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy    331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
          |||||||| || |||||||||||||||||||||||||||||||||||| |||||||||
Db     61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy    391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
          |||||||  ||||| |||||||||||| |||| |||||||||||||| ||||||||||||
Db    121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy    451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
          || || |||||||||||||||| ||||||||| ||||| |||||||||| ||||||||||
Db    181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy    511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCT 570
          |||||||||||  |||||||||| ||||||||| ||||||| |||||| | |  ||||| |||||||||
Db    241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy    571 GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC 630
          ||||| |||||||||||| | |||| || | || ||||| |||| |||||||||||| |||||
Db    301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy    631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
          || |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db    361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy    691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy    751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
          ||||| || |||||||| ||||||||||| |||||||||||||||||||||| |||| || |||
Db    481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy    811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
          ||||||||    |||||||||||||||||| |||||||||||||| || |||||| ||||||
Db    541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy    871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
          || || |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy    931 TACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
          ||||| |||||||| |||||||| ||||| |||||||| |||||||||||||||||||||||||||
Db    661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy    991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
          || |||||| || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy   1051 AGCGCTGCC 1059
          ||||| |||
Db    781 AGCGCCGCC 789
```

RESULT 15
US-09-119-788-1
; Sequence 1, Application US/09119788
; Patent No. 6166193
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,788
; FILING DATE: 21-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-119-788-1

  Query Match   46.1%; Score 511.8; DB 3; Length 1633;
  Best Local Similarity 70.0%; Pred. No. 1e-112;
  Matches 706; Conservative   0; Mismatches 297; Indels   6; Gaps   1;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
            | || || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db   217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
            ||||||| |||||| | || | |||||||||||||| || | || ||| ||||

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Db      277  GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG  336

Qy      200  TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA  259
             |  ||  |||| ||||||        |||||||||||||||||||  |||||||||||||  ||||
Db      337  TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA  396

Qy      260  ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG  319
             |  ||  ||  |||||||| ||  || ||||||     |  |||||| ||  ||||  ||| | ||||
Db      397  ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG  456

Qy      320  ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG  379
             | |||||||||  |||||| |  || ||  ||    |||| |||||  ||  ||  ||||||||||
Db      457  ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA  516

Qy      380  CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG  439
             | ||||| ||||| |||| || | ||  || || ||  ||||   |||  || || |||||||||
Db      517  CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG  576

Qy      440  CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG  499
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Db      577  CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA  636

Qy      500  GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA  559
             |||||||  ||| ||        || ||| | || |||||      |||||| | | ||||||
Db      637  TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA  696

Qy      560  GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG  619
              |||  |  || |   ||||||    ||     ||||  |   | |||  |||| |||||||
Db      697  CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG  756

Qy      620  CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC  679
             | |||   |  |||||||||||||  |||||||   || |||||||  | || || ||| |
Db      757  GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC  816

Qy      680  CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA  739
             ||||| | ||||||||     |||| ||| | || |||||  |||||  ||||||  || | || ||||
Db      817  CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA  876

Qy      740  TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG  799
             |||| || || | |  |||||| | |   | | | || ||||||| ||      |||| |
Db      877  TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT  930

Qy      800  ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG  859
             |  |  |  | ||  |     |   || |||||   ||||    |  |||||||||
Db      931  CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA  990

Qy      860  TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT  919
             | ||||||||| || || | |||||||| ||||| |||| ||||||||||  |||||  ||||| |
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Qy      920  TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT  979
             | || |  ||||| || ||  || || ||  || |  ||| || ||| ||  || ||||||
Db      1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT  1110

Qy      980  TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG  1039
             |  |||  |   |||  |  || |||| || ||||| |  ||||| || |||||||||| |
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Qy      1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
             |  ||  |||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||  |||||||||
Db      1171 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1219
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Search completed: October 15, 2004, 22:55:08
Job time : 90.0094 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 572.496 Seconds
                                             (without alignments)
                                             9829.265 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc.........ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query

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No.    Score  Match Length DB   ID                      Description
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   1   1110   100.0  1110  10   US-09-393-696-3         Sequence 3, Appli
   2   1102    99.3  1110  14   US-10-077-874-3         Sequence 3, Appli
   3   1079.4  97.2  1564  15   US-10-225-567A-367      Sequence 367, App
   4   1079.4  97.2  1564  16   US-10-352-684A-21       Sequence 21, Appl
   5   1077.8  97.1  1209  10   US-09-393-696-1         Sequence 1, Appli
   6   1077.8  97.1  1209  14   US-10-077-874-1         Sequence 1, Appli
   7   1077.8  97.1  1564   9   US-09-828-538-23        Sequence 23, Appl
   8   1075.2  96.9  1116  14   US-10-077-874-5         Sequence 5, Appli
   9   1075.2  96.9  1133  10   US-09-393-696-5         Sequence 5, Appli
  10   1074.6  96.8  1278  11   US-09-826-509-548       Sequence 548, App
  11    905    81.5  1281   9   US-09-730-931-1         Sequence 1, Appli
  12    661    59.5   789  15   US-10-278-087A-55       Sequence 55, Appl
  13    511.8  46.1  1633  15   US-10-282-717-1         Sequence 1, Appli
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  17    241.2  21.7 10453   9   US-09-828-538-21        Sequence 21, Appl
  18    236    21.3   244   9   US-09-828-538-6         Sequence 6, Appli
  19    223.8  20.2   227   9   US-09-828-538-10        Sequence 10, Appl
  20    199    17.9   356   9   US-09-828-538-2         Sequence 2, Appli
  21    179    16.1   179   9   US-09-828-538-4         Sequence 4, Appli
  22    161.6  14.6  1290  17   US-10-719-587-55        Sequence 55, Appl
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  25    161.6  14.6  1293  15   US-10-225-567A-657      Sequence 657, App
  26    161.6  14.6  1320   9   US-09-292-973-3         Sequence 3, Appli
  27    154.6  13.9  1299  17   US-10-719-587-38        Sequence 38, Appl
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  30    126    11.4   977  12   US-09-876-143-1561      Sequence 1561, Ap
  31    122    11.0   122   9   US-09-828-538-12        Sequence 12, Appl
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  33    119    10.7  1174  17   US-10-611-210-9         Sequence 9, Appli
  34    117.4  10.6  1110  14   US-10-044-592-17        Sequence 17, Appl
  35    117.4  10.6  1110  15   US-10-278-087A-31       Sequence 31, Appl
  36    117.4  10.6  1113  15   US-10-225-567A-244      Sequence 244, App
  37    117.4  10.6  1152  17   US-10-611-210-10        Sequence 10, Appl
  38    117.4  10.6  1174  17   US-10-611-210-7         Sequence 7, Appli
  39    117.4  10.6  1331  14   US-10-044-592-73        Sequence 73, Appl
  40    116.8  10.5  1173  17   US-10-611-210-6         Sequence 6, Appli
  41    116    10.5   116   9   US-09-828-538-8         Sequence 8, Appli
  42    114.2  10.3  1174  17   US-10-611-210-8         Sequence 8, Appli
  43    105.6   9.5   669  14   US-10-044-592-70        Sequence 70, Appl
c 44    104     9.4   436  13   US-10-027-632-275272    Sequence 275272,
c 45    104     9.4   436  16   US-10-027-632-275272    Sequence 275272,
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ALIGNMENTS

RESULT 1
US-09-393-696-3
; Sequence 3, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:

Query Match   100.0%;   Score 1110;   DB 10;   Length 1110;
Best Local Similarity   100.0%;   Pred. No. 9.1e-303;
Matches 1110; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||·||||||||||||||||||||||||||||||||||||
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Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||┼┼┼|||||||||||||||||||||||||||||||||||||
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Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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RESULT 2
US-10-077-874-3
; Sequence 3, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD

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    Query Match                  99.3%;  Score 1102;  DB 14;  Length 1110;
    Best Local Similarity        99.5%;  Pred. No. 1.6e-300;
    Matches 1105;  Conservative     0;  Mismatches     5;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy     601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy    1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db    1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 3
US-10-225-567A-367
; Sequence 367, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 367
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-367

  Query Match   97.2%; Score 1079.4; DB 15; Length 1564;
  Best Local Similarity 99.4%; Pred. No. 4.2e-294;
  Matches 1083; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

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;  APPLICANT:  Weich, Nadine S.
;  APPLICANT:  Kelly, Louise M.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,
;  TITLE OF INVENTION:  15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
;  TITLE OF INVENTION:  1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,
;  TITLE OF INVENTION:  15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
;  FILE REFERENCE: MPI02-019P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/352,684A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/354,333
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/360,258
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/364,476
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/375,626
;  PRIOR FILING DATE: 2002-04-26
;  PRIOR APPLICATION NUMBER: US 60/386,494
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/390,965
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: US 60/392,480
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: US 60/394,128
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,783
;  PRIOR FILING DATE: 2002-07-31
;  PRIOR APPLICATION NUMBER: US 60/403,221
;  PRIOR FILING DATE: 2002-08-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS:. 62
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)...(1431)
US-10-352-684A-21
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   Query Match              97.2%;  Score 1079.4;  DB 16;  Length 1564;
   Best Local Similarity    99.4%;  Pred. No. 4.2e-294;
   Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db    274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                ||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
                ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGGC 1089
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Db    1234 CTCAGTGGC 1242
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RESULT 5
US-09-393-696-1
; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1209)
US-09-393-696-1

    Query Match   97.1%;   Score 1077.8; DB 10; Length 1209;
    Best Local Similarity 99.4%;   Pred. No. 1.1e-293;
    Matches 1082; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                      ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                      ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                      ·||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                      || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
                      |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGGC 1089
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RESULT 6
US-10-077-874-1
; Sequence 1, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1209 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1209
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-874-1

    Query Match   97.1%;   Score 1077.8;   DB 14;   Length 1209;
    Best Local Similarity 99.4%;   Pred. No. 1.1e-293;
    Matches 1082; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
         ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy   601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
         |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy   781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
```

```
Qy         901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
               ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy         961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy        1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy        1081 CTCAGTGGC 1089
               |||||||||
Db        1081 CTCAGTGGC 1089


RESULT 7
US-09-828-538-23
; Sequence 23, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
;   APPLICANT: Ellis, Catherine E.
;   APPLICANT:  Kwok, Cheni
;   APPLICANT:  Bodsworth, Nicola J.
;   APPLICANT:  Halsey, Wendy
;   APPLICANT:  Van Horn, Stephanie
;   TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
;   TITLE OF INVENTION:  of Use Thereof in Diagnostic Applications
;   FILE REFERENCE: GH-50038-C1
;   CURRENT APPLICATION NUMBER: US/09/828,538
;   CURRENT FILING DATE:  2001-04-06
;   PRIOR APPLICATION NUMBER: 60/088,624
;   PRIOR FILING DATE: 1998-06-08
;   PRIOR APPLICATION NUMBER: 60/093,726
;   PRIOR FILING DATE: 1998-07-22
;   PRIOR APPLICATION NUMBER: 09/328,014
;   PRIOR FILING DATE: 1999-06-08
;   NUMBER OF SEQ ID NOS: 24
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-828-538-23

  Query Match            97.1%;   Score 1077.8;  DB 9;   Length 1564;
  Best Local Similarity  99.4%;   Pred. No. 1.2e-293;
  Matches 1082;  Conservative   0;  Mismatches   7;  Indels    0;  Gaps    0;

Qy           1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy          61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 273
```

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Qy    121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC  333

Qy    181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  393

Qy    241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  453

Qy    301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  513

Qy    361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  573

Qy    421  CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  633

Qy    481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  693

Qy    541  GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
           |||||||||   |||  ||||||||||||||||||||||||||||||||||||||||||||
Db    694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  753

Qy    601  CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
           |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy    661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy    721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT  960
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113
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Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          |·|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy   1081 CTCAGTGGC 1089
          |||||||||
Db   1234 CTCAGTGGC 1242
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RESULT 8
US-10-077-874-5
; Sequence 5, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1116 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1116
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     Query Match              96.9%;   Score 1075.2;  DB 14;  Length 1116;
     Best Local Similarity    99.3%;   Pred. No. 5.9e-293;
     Matches 1080;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088


RESULT 9
US-09-393-696-5
; Sequence 5, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc. et al.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   FILE REFERENCE: PF168P2
;   CURRENT APPLICATION NUMBER: US/09/393,696
;   CURRENT FILING DATE: 1999-09-10
;   EARLIER APPLICATION NUMBER: PCT/US95/05616
;   EARLIER FILING DATE: 1995-05-05
;   EARLIER APPLICATION NUMBER: US08/462,509
;   EARLIER FILING DATE: 1995-06-05
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1131)
US-09-393-696-5

  Query Match            96.9%;  Score 1075.2;  DB 10;  Length 1133;
  Best Local Similarity   99.3%;  Pred. No. 6e-293;
  Matches 1080;  Conservative    0;  Mismatches   8;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ·|||||||||||||||||||||||||||||||||||||,||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          ||||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||  |||||||||||||||||||||||||||||||||·||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
             ||||||||
Db      1081 CTCAGTGG 1088


RESULT 10
US-09-826-509-548
; Sequence 548, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT:  Liaw, Chen W.
; APPLICANT:  Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
; TITLE OF INVENTION:  Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE:  2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 548
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-826-509-548

  Query Match           96.8%;  Score 1074.6;  DB 11;  Length 1278;
  Best Local Similarity  99.2%;  Pred. No. 9e-293;
  Matches 1080;  Conservative   0;  Mismatches   9;  Indels   0;  Gaps   0;

Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy    1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy    1081  CTCAGTGGC 1089
            |||||||||
Db    1081  CTCAGTGGC 1089


RESULT 11
US-09-730-931-1
; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
;    APPLICANT:  ELLIS, CATHERINE E.
;    TITLE OF INVENTION:  DOG OREXIN 1 RECEPTOR
;    FILE REFERENCE:  GH-70669
;    CURRENT APPLICATION NUMBER: US/09/730,931
;    CURRENT FILING DATE:  2000-12-06
;    PRIOR APPLICATION NUMBER:  60/169,373
;    PRIOR FILING DATE:  1999-12-07
;    NUMBER OF SEQ ID NOS:  2
;    SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;    LENGTH: 1281
;    TYPE: DNA
;    ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

    Query Match            81.5%;   Score 905;  DB 9;  Length 1281;
    Best Local Similarity  89.9%;   Pred. No. 6.2e-245;
    Matches  984;  Conservative   0;  Mismatches 105;  Indels   6;  Gaps   1;

Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
           |||||||||||||||||||||||||||||||||||| |||  |||| | ||| || | |||| |
Db       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGACTGGGACCCCCACCGGCGGCGGGGAGCTG 60

Qy      61 TCCCCT------GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
           || ||       ||||||||| |||||||||| ||||| || |||||||||||||| |||
Db      61 TCTCCGTCACTGGTGCCTCCCGACTATGAAGACGAGTTCCTGCGCTATCTGTGGCGCGAT 120

Qy     115 TATCTGTACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTC 174
           || |||||||||| |||||||||||||||||||||||||||| ||||| |||||||||||| |
Db     121 TACCTGTACCCAAAGCAGTATGAGTGGGTCCTCATCGCTGCCTACGTGGCTGTGTTCCTA 180

Qy     175 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGG 234
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     181 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGAGGAACCACCACATGAGG 240

Qy     235 ACAGTCACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATC 294
           || |||||||||| |||||||||||||||||||||||||| || ||||||||| || |||
Db     241 ACGGTCACCAACTATTTCATTGTCAACCTGTCCCTGGCTGATGTGCTGGTGACAGCCATC 300

Qy     295 TGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTC 354
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            |||||  |||||||||||||||||||  |||||||||||||||||||||||  |||||| ||| |||||
Db      301 TGCCTCCCGGCCAGCCTGCTGGTAGACATCACTGAGTCCTGGCTCTTCGGTCATACCCTC 360

Qy      355 TGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGC 414
            |||||| ||||||||||||  |||||||||  ||||||  |||||| |||||||||||||| ||||||||||
Db      361 TGCAAAGTCATCCCCTACCTACAGGCCGTGTCTGTGTCGGTGGCAGTGCTGACTCTCAGC 420

Qy      415 TTCATCCCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCC 474
            ||||||  ||||||||||||||||||||||||||||||||||| || |||||||||||||| |||
Db      421 TTCATCGCCCTGGACCGCTGGTATGCCATCTGCCACCCGCTGTTGTTCAAGAGCACCGCC 480

Qy      475 CGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCC 534
            ||||| |||||  |||||||||||||||||||||||||||||  ||||  ||||||| ||
Db      481 CGGCGCGCCCGCAGCTCCATCCTGGGCATCTGGGCTGTGTCATTGGCTGTCATGGTACCT 540

Qy      535 CAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTC 594
            ||||||||  |||||| ||| |||||||  |||||  |||||||||||||||||||||| || |||
Db      541 CAGGCTGCCGTCATGGAATGCAGCAGCGTGCTCCCTGAGCTAGCCAACCGCACCCGCCTC 600

Qy      595 TTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 654
            |||||  | ||| |||||||  ||||||||||||||||||||||||||||||||||||||||
Db      601 TTCTCTGTGTGTGATGAACACTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 660

Qy      655 TTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATA 714
            |||||  |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db      661 TTCTTCATTGTCACCTACTTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATC 720

Qy      715 TTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGG 774
            ||||||||||||||||||||||||||||||| |||||||| || || ||||||| ||||||||
Db      721 TTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGCACCACATCGGCCCTGGTGAGGAACTGG 780

Qy      775 AAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCC 834
            ||||| |||||| |||||||||| ||||| || ||  ||||||| |  || |||| ||
Db      781 AAGCGGCCCTCGGACCAGCTGGAGGACCAGGGGCCCGGCCTGAGCGCGGAACCCCCCCCT 840

Qy      835 CGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAG 894
            ||||  ||| ||||||||||||||| |||||||||||||| || |||||||||| ||||||
Db      841 CGGGGCCCGGGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCGCGGAGGAAGACGGCCAAG 900

Qy      895 ATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAAT 954
            |||||||||||| ||||||||||| ||||||||||||||||||| |||||||| ||||||||
Db      901 ATGCTGATGGTGCTGCTGCTGGTCTTTGCCCTCTGCTACCTGCCCATCAGTGTCCTCAAT 960

Qy      955 GTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC 1014
            |||||  |||||||||||||||||||||||||||  |||||||||| |||||  | ||||||
Db      961 GTCCTCAAGAGGGTGTTCGGGATGTTCCGCCAATCCAGTGACCGAGAAGCCGTGTACGCC 1020

Qy     1015 TGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTAC 1074
            ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db     1021 TGCTTCACCTTCTCCCACTGGCTGGTGTATGCCAACAGCGCTGCCAACCCCATCATCTAC 1080

Qy     1075 AACTTCCTCAGTGGC 1089
            |||||||||| |||
Db     1081 AACTTCCTCAGCGGC 1095
```

RESULT 12

US-10-278-087A-55

;   GENERAL INFORMATION:
;   APPLICANT: Shuji Hinuma
;   Yasuaki Ito
;   Ryo Fujii
;   TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;   Production, And Use Thereof
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Edwards & Angell, LLP
;   STREET: 101 Federal Street
;   CITY: BOSTON
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02209
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/278,087A
;   FILING DATE: 31-Jan-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/461,436
;   FILING DATE: 14-DEC-1999
;   APPLICATION NUMBER: 09/038,572
;   FILING DATE: 11-MAR-1998
;   APPLICATION NUMBER: 08/513,974
;   FILING DATE: 14-SEP-1995
;   APPLICATION NUMBER: PCT/JP95/01599
;   FILING DATE: 10-AUG-1995
;   APPLICATION NUMBER: 7-093989
;   FILING DATE: 19-APR-1995
;   APPLICATION NUMBER: 7-057186
;   FILING DATE: 16-MAR-1995
;   APPLICATION NUMBER: 7-007177
;   FILING DATE: 20-JAN-1995
;   APPLICATION NUMBER: 6-326611
;   FILING DATE: 28-DEC-1994
;   APPLICATION NUMBER: 6-270017
;   FILING DATE: 02-NOV-1994
;   APPLICATION NUMBER: 6-236357
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-236356
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-189274
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189273
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189272
;   FILING DATE: 11-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: CONLIN, DAVID G.

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   Query Match              59.5%;   Score 661;  DB 15;   Length 789;
   Best Local Similarity    89.9%;   Pred. No. 3.6e-176;
   Matches  709;  Conservative   0;  Mismatches   80;  Indels   0;  Gaps   0;

Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || ||||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              ||||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              |||||||   ||||| |||||||||| |||| |||||||||||||| ||||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
              || || ||||||||||||||||| ||||||||| |||||| |||||||||||| |||||||||||
Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCT 570
              ||||||||||| ||||||||||| ||||||||| ||||| || ||||| |||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC 630
              ||||| ||||||||||| || ||| | || ||||| |||| |||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || ||||||||||||||||||| |||||||| |||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || ||||||||| |||||||||||| |||||||||||||||| ||||| || |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||   |||||||||||||||| ||||||||||||||||| || ||||| || |||
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Db      541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy      871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
                || ||  |||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db      601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy      931 TACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
                |||||  |||||||||  |||||||||  |||||  |||||||||  |||||||||||||||||||||
Db      661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy      991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
                ||  ||||| || ||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy     1051 AGCGCTGCC 1059
                ||||| |||
Db      781 AGCGCCGCC 789


RESULT 13
US-10-282-717-1
; Sequence 1, Application US/10282717
; Publication No. US20030083466A1
; GENERAL INFORMATION:
;   APPLICANT: YANAGISAWA, MASASHI
;   TITLE OF INVENTION: cDNA CLONE MY1 THAT ENCODES A NOVEL
;   TITLE OF INVENTION:  HUMAN 7-TRANSMEMBRANE RECEPTOR
;   FILE REFERENCE: GH50029D1C1
;   CURRENT APPLICATION NUMBER: US/10/282,717
;   CURRENT FILING DATE:  2002-10-28
;   PRIOR APPLICATION NUMBER: 09/676,625
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: 09/119,788
;   PRIOR FILING DATE: 1998-07-21
;   PRIOR APPLICATION NUMBER: 60/053,790
;   PRIOR FILING DATE: 1997-07-25
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1633
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-282-717-1

   Query Match              46.1%;   Score 511.8;  DB 15;   Length 1633;
   Best Local Similarity   70.0%;   Pred. No. 5.2e-134;
   Matches  706;  Conservative    0;  Mismatches  297;  Indels    6;  Gaps    1;

Qy       80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
                |  || ||  ||  ||  ||  ||  ||  ||  ||  ||||||| |  ||  ||  ||| ||||  |||  |  |||||||
Db      217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy      140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
                |||||||  ||||||  |   ||   |       |||||||||||||  ||  |  ||  |||      ||||
Db      277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy      200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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              |  ||   ||||  ||||||   |||||||||||||||||||||  || |||||||||||||||  ||||
Db     337 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 396

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              |  || ||  ||||||||| || || |||||    | |||||| || |||| ||| | ||||
Db     397 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 456

Qy     320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              | |||||||||| ||||||  | || || ||  |||| |||||  ||  || || |||||||||||
Db     457 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 516

Qy     380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              | |||||  ||||| ||| |  | || ||  || |||| |||  || |||| || ||||||||
Db     517 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 576

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              | |||||| ||||||    |  |||| ||||||||||||    |||||||||  |   |||  |
Db     577 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 636

Qy     500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
              ||||||| ||| ||     || ||| | || |||||    |||||| | | ||||||
Db     637 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 696

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
              ||| | || |   |||||||  || |     |||||   |  | ||| |||| |||||||
Db     697 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 756

Qy     620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  |  ||||||||||||| |||||| || |||||  | || || ||| |||| |
Db     757 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 816

Qy     680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
              ||||| | |||||||    |||| ||| | || |||||| |||||| | || ||||
Db     817 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 876

Qy     740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
              ||||  ||  ||  | || | | |    | |  | | |||||||| ||      |||| |
Db     877 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 930

Qy     800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
              | |   |   || |    |     | || |||||  |||| |   | ||||||
Db     931 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA 990

Qy     860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              | ||||||| || || |  |||||| |||||| |||| ||||||| |||||  ||| |
Db     991 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1050

Qy     920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | || | |||||| || || || ||  ||||||||||||| || ||||| || || |||||||
Db    1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1110

Qy     980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              |    ||| |     ||| | | || |||| ||||| || ||||| || ||||| || |||||||| |
Db    1111 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1170

Qy    1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
              | || ||||| || ||||| || || || || || || || || ||||||||
```

RESULT 14
US-10-225-567A-369
; Sequence 369, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 369
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-369

    Query Match   46.1%;   Score 511.8; DB 15;   Length 1843;
    Best Local Similarity 70.0%;   Pred. No. 5.3e-134;
    Matches 706; Conservative   0; Mismatches 297; Indels   6; Gaps   1;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
            | || || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db   428 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 487

Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
            ||||||| ||||| | || | |||||||||||||| || | || ||| ||||
Db   488 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 547

Qy   200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
            | || |||| |||||| |||||||||||||||||||| || ||||||||||||||| ||||
Db   548 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 607

Qy   260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
            | || || |||||||| || || ||||| | |||||| || |||| ||| | ||||
Db   608 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 667

Qy   320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
            | ||||||||| |||||| | || || || |||| ||||| || || || |||||||||
Db   668 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 727

Qy   380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
            | |||||| ||||| ||| | || || || || |||| .||| || |||| || |||||||
Db   728 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 787

Qy   440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
            | |||||| ||||| | |||| |||||||||||| |||||||||| ·| ||| |

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Db    788 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 847

Qy    500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
              ||||||| ||| || || ||| | || ||||| |||||| | | |||||
Db    848 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 907

Qy    560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
              ||| | || | ||||||| || ||||| | | ||| |||| |||||||
Db    908 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 967

Qy    620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  | |||||||||||| |||||||  || |||||| | || || ||| |||| |
Db    968 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 1027

Qy    680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
              ||||| | ||||||| |||| ||| | || ||||| ||||| ||||||| | || ||||
Db   1028 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 1087

Qy    740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
              |||| || || | || | | | | || | || |||||||| ||        |||| |
Db   1088 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 1141

Qy    800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
              | | | | ||| | | || |||||    |||| |  ||||||||
Db   1142 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 1201

Qy    860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              | ||||||||| || ||  | |||||| |||||| |||| ||||||| ||||| |||| |
Db   1202 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1261

Qy   . 920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | ||  | ||||||| || || || ||| |||||||||||| || ||||| || || |||||||
Db   1262 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1321

Qy    980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              |   ||| |   ||| | ||  |||| || ||||| || ||||| || |||||||| |
Db   1322 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1381

Qy   1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
              | || |||||| || ||||| || || || || || || || ||||||||
Db   1382 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1430
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RESULT 15
US-09-826-509-550
; Sequence 550, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
;   APPLICANT: Lehmann-Bruinsma, Karin
;   APPLICANT: Liaw, Chen W.
;   APPLICANT: Lin, I-Lin
;   TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
;   TITLE OF INVENTION: Protein-Coupled Receptors
;   FILE REFERENCE: AREN-207
;   CURRENT APPLICATION NUMBER: US/09/826,509
;   CURRENT FILING DATE: 2001-04-05

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  Query Match          45.7%;  Score 507;  DB 11;  Length 1335;
  Best Local Similarity 69.7%;  Pred. No. 1.1e-132;
  Matches  703;  Conservative   0;  Mismatches  300;  Indels   6;  Gaps    1;


Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       104 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163


Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| |||||| | || |       ||||||||||||| || | || |||    ||||
Db       164 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 223


Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||  |||| |||||| |||||||||||||||||||||||| || ||||||||||||| ||||
Db       224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283


Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || |||||||| || || ||||     | |||||| || |||| ||| | ||||
Db       284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343


Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | ||||||||| |||||| | || || || || |||| ||||| || || || |||||||||
Db       344 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 403


Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
             | |||||| |||||| ||| | | || || || || |||| ||| || |||| || |||||||
Db       404 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 463


Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | |||||| |||||    |||| ||||||||||||||||     |||||||||| | ||| |
Db       464 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523


Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
               |||||| ||| ||      || ||| | || ||||| ||||||- ||| |||||
Db       524 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 583


Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
                ||| | || |     ||||||| ||    ||||| | | ||| |||| |||||||
Db       584 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643


Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
             | |||   | ||||||||||| ||||| || || |||||| | || || ||| |||| |
Db       644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 703


Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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                      |||||  |  ||||||||      ||||  |||  |  ||  |||||  |||||  ||||||  |  ||  ||||
Db    704 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 763

Qy    740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
                      ||||  ||  ||   |  ||  |  | |      |   |  ||  ||||||||  ||           ||||    |
Db    764 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 817

Qy    800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
                       |  |       |  ||  |       |       |  ||  |||||      ||||   |      |||||||
Db    818 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 877

Qy    860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
                       |  |||||||||  ||  ||    |  |||||  |||          ||||  |||||||  |||||      ||||  |
Db    878 TAAAGCAGATCCGAGCCAGAAGGAAAACAAAACGGATGTTGATGGTTGTGCTTTTGGTAT 937

Qy    920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
                       |  ||   |  |||||  ||  ||  ||  |||  |||||||||||  ||  |||||  ||  ||  ||||||||
Db    938 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 997

Qy    980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
                       |      |||      |        |||   |  ||    ||||  ||  |||||  ||  |||||  ||  |||||||||  |
Db    998 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1057

Qy   1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
                       |  ||  |||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||  |||||||||
Db   1058 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1106


Search completed: October 16, 2004, 03:40:42
Job time : 575.496 secs
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